

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:02 ; Search time 10.338 Seconds

(without alignments)  
1055.158 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357

Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALLKYVNGTCQCT 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1096.5	80.8	261	1	RIP3_PHYAM
2	1050	77.4	313	1	RIP1_PHYAM
3	1014.5	74.8	294	1	RIP1_PHYAM
4	453	33.4	310	1	RIP2_PHYAM
5	342	25.2	299	1	RIP6_SAPOR
6	337	24.8	253	1	RIP5_SAPOR
7	336	24.8	253	1	RIP7_SAPOR
8	335.5	24.7	292	1	RIP2_SAPOR
9	319.5	23.5	293	1	RIP0_DIACA
10	313	23.1	316	1	RIP3_GELMU
11	291	21.4	576	1	RIC1_RICCO
12	287.5	21.2	294	1	RIP1_TRIAN
13	283	20.9	236	1	RIP3_SAPOR
14	271.5	20.0	564	1	ACGL_RICCO
15	260	19.2	282	1	RIP2_BRVDI
16	257	18.9	278	1	RIP2_MIRJA
17	250	18.4	286	1	RIP1_CUCPT
18	247.5	18.2	286	1	RIP1_MOMCH
19	241	17.8	289	1	RIP5_TRIKI
20	240	17.7	289	1	RIP1_TRIKI
21	235	17.3	250	1	RIP8_LUCFY
22	233.5	17.2	563	1	NIGB_SAMNI
23	230.5	17.0	528	1	ABRA_ABRPR
24	229	16.9	527	1	ABRA_ABRPR
25	225	16.6	290	1	RIP1_BRVDI
26	215	15.8	286	1	RIP2_MOMBA
27	209.5	15.4	562	1	ABRC_ABRPR
28	200	14.7	254	1	MLA_VISAL
29	199.5	14.7	277	1	RIP4_LUCFY
30	199.5	14.7	277	1	RIP4_SAPOR
31	199.5	14.7	277	1	RIP4_SAPOR
32	199.5	14.7	277	1	RIP4_SAPOR
33	199.5	14.7	277	1	RIP4_SAPOR
34	199.5	14.7	277	1	RIP4_SAPOR
35	199.5	14.7	277	1	RIP4_SAPOR
36	199.5	14.7	277	1	RIP4_SAPOR
37	199.5	14.7	277	1	RIP4_SAPOR
38	199.5	14.7	277	1	RIP4_SAPOR
39	199.5	14.7	277	1	RIP4_SAPOR
40	199.5	14.7	277	1	RIP4_SAPOR
41	199.5	14.7	277	1	RIP4_SAPOR
42	199.5	14.7	277	1	RIP4_SAPOR
43	199.5	14.7	277	1	RIP4_SAPOR
44	199.5	14.7	277	1	RIP4_SAPOR
45	199.5	14.7	277	1	RIP4_SAPOR

34	119.5	8.8	319	1	SLTA_BP933
35	119	8.8	300	1	RIP3_MAIZE
36	112.5	8.3	280	1	RIP2_HORVU
37	111	8.2	343	1	YOC7_CAEFL
38	110	8.1	560	1	J160_HORVU
39	109.5	8.1	280	1	RIP1_HORVU
40	105.5	7.8	301	1	RIP9_MAIZE
41	103	7.6	304	1	RIP9_MAIZE
42	97.5	7.2	485	1	HXA_YEAST
43	92.5	6.8	303	1	ALB3_MAIZE
44	92.5	6.8	484	1	Y6Z2_METJA
45	91	6.7	511	1	UDPG_DICDI

## ALIGNMENTS

RESULT 1	ID	RIP3_PHYAM	STANDARD:	PRT:	261 AA..
AC	P23339				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Antiviral protein S (PAP-S) (Ribosome-inactivating protein) (RNA				
DE	N-glycosidase) (EC 3.2.2.22).				
OS	Phytolacca americana (Common pokeweed) (Virginian pokeweed).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.				
OX	NCBI_TaxID=3527;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=seed;				
RA	MEDLINE=91242096; PubMed=1368643;				
RA	Kung S.S., Kimura M., Funatsu G.;				
RT	"The complete amino acid sequence of antiviral protein from the seeds				
RT	of pokeweed (Phytolacca americana).";				
RL	Agric. Biol. Chem. 54:3301-3318(1990).				
CC	-1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN				
CC	SYNTHESIS IN VITRO.				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one				
CC	specific adenosine on the 28S rRNA.				
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.				
CC	TYPE 1 RIP SUBFAMILY.				
DR	PIR: J0401; J0401.				
DR	HSSP: 003464; IAPA.				
DR	InterPro: IPR001574; RIP.				
DR	Pfam: PF00161; RIP. 1.				
DR	PRINTS: PR00396; SHIGARICIN.				
DR	PROSITE: PS00275; SHIGA_RICIN; 1.				
KW	Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;				
KW	Toxin.				
FT	ACT_SITE 175 175 BY SIMILARITY.				
FT	DISULFID 34 258				
FT	DISULFID 84 105				
SO	SEQUENCE 261 AA; 29200 MW; D88B99962FE8399D CRC64;				
Query Match	80.8%; Score 1096.5; DB 1; Length 261;				
Best Local Similarity	82.8%; Pred. No. 2.8e-83;				
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;					
OY	2 INTITFDAGNATINKYATFMSLRQADPKIKCYGIPMLPTNTSPKLYLVKIQGNLK 61				
DB	1 INTITFDAGNATINKYATFMSLRQADPKIKCYGIPMLPTNTSPKLYLVKIQGNLK 60				
OY	62 TTTLMLRNRLVYMGSDPFGNCKRYHFNDFITSPERDVNTLSSSSRVAMSNYN 121				
DB	61 TTTLMLRNRLVYMGSDPFGNCKRYHFNDFITSPERDVNTLSSSSRVAMSNYN 119				
OY	122 SLPTMEKKAEEVSNQVQLGIQLSSDGKISGVDFPVKTEAFLLVAIQVSEAFK 181				
DB	120 GLYPTLEKKAGVTSRNEVQLGIQLSSDGKISGVDFPVKTEAFLLVAIQVSEAFK 179				

```

OY 182 KYIENOVKTNNRAFYDDPVYINLEEKWGISAIHNKAGCALPKPELYDAKGTKNIVL 241
    |||||
Db 180 KYIENOVKTNNRDFSPNDKVLDEENMGKISTAIHNSKNALPKPELKNADGTKNIVL 239
    |||||
OY 242 RVDEINRDVALLKRVNCTCQT 263
    |||||
Db 240 RVDEIKPDVGLNLNVNCTCOAT 261
    |||||

RESULT 2
RIP1-PHYAM STANDARD: PRT: 313 AA.
ID RIP1-PHYAM
AC P10297;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein I precursor (PAP-1) (PAP-C) (Ribosome-inactivating
DE protein) (tRNA N-glycosidase) (EC 3.2.2.22).
GN PAI.
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllales: Caryophyllaceae: Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 23-62.
RC TISSUE-Leaf:
RX MEDLINE=92003676; PubMed=1912488;
RA Lin Q., Chen Z.C., Antoniw J.F., White R.F.;
RT "Isolation and characterization of a cDNA clone encoding the
RL anti-viral protein from Phytolacca americana."
RN [2]
RP SEQUENCE OF 23-65.
RX MEDLINE=89193489; PubMed=2930487;
RA Barbieri L., Bolognesi A., Cenni P., Falasca A.I., Minghetti A.,
RA Gaetano L., Guicciardi A., Lepi D., Miller S.P.;
RT "Ribosome-inactivating proteins from plant cells in culture."
RL Biochem. J. 257:801-807(1989).
RN [3]
RP SEQUENCE OF 23-54.
RC TISSUE-Leaf:
RX MEDLINE=83290867; PubMed=6885760;
RA Houston L.L., Ramakrishnan S., Hermodson M.A.;
RT "Seasonal variations in different forms of pokeweed antiviral protein,
RT a potent inactivator of ribosomes."
RL J. Biol. Chem. 258:9601-9604(1983).
RN [4]
RP SEQUENCE OF 23-54.
RC TISSUE-Leaf:
RX MEDLINE=85023392; PubMed=6091760;
RA Bjorn M.J., Larrick J., Platak M., Wilson K.J.;
RT "Characterization of translational inhibitors from Phytolacca
RT americana: amino-terminal sequence determination and antibody-
RL inhibitor conjugates."
RN [5]
RP SEQUENCE OF 23-54.
RC TISSUE-Root:
RX MEDLINE=91064383; PubMed=2248976;
RA Bolognesi A., Barbieri L., Abbondanza A., Falasca A.I., Carnicelli D.,
RA Battelli M.G., Stipe F.;
RT "Purification and properties of new ribosome-inactivating proteins
RT with RNA N-glycosidase activity."
RL Biochim. Biophys. Acta 1087:293-302(1990).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94016586; PubMed=841176;
RA Monzingo A.F., Collins E.J., Ernst S.R., Irvin J.D., Robertus J.D.;
RT "The 2.5 A structure of pokeweed antiviral protein."
RL J. Mol. Biol. 233:705-715(1993).
RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-284.
RX MEDLINE=99421320; PubMed=10493577;
RA Kurinov I.V., Myers D.E., Irvin J.D., Uckun F.M.;
RT "X-ray crystallographic analysis of the structural basis for the
RT interactions of pokeweed antiviral protein with its active site
RL inhibitor and ribosomal RNA substrate analogs."
CC Protein Sci. 8:1765-1772(1999).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
CC SYNTHESIS IN VITRO.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- TISSUE SPECIFICITY: SPRING LEAVES AND ROOTS.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X53583; CAA39054.1;
DR PIR: S02792; S02792.
DR PIR: S13469; S13469.
DR PDB: 1PAF; 31-JAN-94.
DR PDB: 1PAC; 31-JAN-94.
DR PDB: 1QCI; 15-SEP-99.
DR PDB: 1QCG; 15-SEP-99.
DR PDB: 1QCF; 15-SEP-99.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PRO0396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Plant defense: Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal; 3D-structure.
FT CHAIN 1 23 285
FT PROPEP 286 313
FT ACT_SITE 198 198
FT DISULFID 56 281
FT STRAND 107 128
FT HELIX 25 29
FT STRAND 35 49
FT STRAND 55 56
FT TURN 57 58
FT STRAND 59 61
FT TURN 65 66
FT STRAND 71 78
FT HELIX 79 81
FT STRAND 82 89
FT TURN 90 93
FT STRAND 94 102
FT TURN 103 105
FT STRAND 106 112
FT TURN 113 114
FT TURN 117 117
FT HELIX 118 127
FT TURN 131 132
FT STRAND 134 136
FT STRAND 139 139
FT HELIX 145 152
FT TURN 153 153
FT TURN 157 158
FT STRAND 162 162
FT HELIX 164 174
FT TURN 175 176
FT HELIX 182 195
FT TURN 196 196
FT HELIX 197 201
FT TURN 203 211
FT HELIX 214

```

```

CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Cell wall.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/isb-ch).
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D10600; BAA01451.1; -.
CC PIR: S28421; S28421.
CC PDB: IAPA; 3I-JAN-94.
CC InterPro: IPR001574; RIP.
CC Pfam: PF00161; RIP: 1.
CC DR PROSITE: PS00275; SHIGA_RICIN; 1.
CC KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
CC Toxin; Signal; Cell wall; 3D-structure.
CC FT SIGNAL 1 24
CC FT CHAIN 25 285
CC FT PROPEP 286 294
CC FT ACT_SITE 199 199
CC FT DISULFID 38 282
CC FT DISULFID 108 130
CC FT STRAND 28 31
CC FT HELIX 32 34
CC FT HELIX 37 51
CC FT STRAND 57 58
CC FT TURN 59 60
CC FT STRAND 61 63
CC FT TURN 67 68
CC FT STRAND 73 79
CC FT TURN 81 82
CC FT STRAND 85 91
CC FT TURN 92 94
CC FT STRAND 97 104
CC FT TURN 105 106
CC FT STRAND 107 113
CC FT TURN 114 115
CC FT HELIX 119 129
CC FT STRAND 136 138
CC FT STRAND 141 141
CC FT HELIX 147 154
CC FT TURN 155 155
CC FT HELIX 158 160
CC FT STRAND 163 163
CC FT HELIX 165 175
CC FT TURN 176 177
CC FT TURN 183 195
CC FT HELIX 196 197
CC FT TURN 198 202
CC FT HELIX 204 212
CC FT TURN 213 215
CC FT STRAND 218 218
CC FT HELIX 222 240
CC FT TURN 242 242
CC FT STRAND 243 244
CC FT STRAND 245 253
CC FT TURN 255 256
CC FT STRAND 259 264
CC FT HELIX 265 271
CC FT STRAND 275 275
CC SEQUENCE 294 AA; 33069 MW; F2EC27724FA85596 CRC64;
Query Match 74.8%; Score 1014.5; DB 1; Length 294;
Best Local Similarity 76.8%; Pred. No. 1.9e-76;
Matches 202; Conservative 37; Mismatches 37; Indels 3; Gaps 3;
2 INTFTDAGNATINKYATFMESLRNOKDPRKICYGIPLMDTNTSTPKYLIVKLOGANLK 61

```

```

Db 25 INTTFDGNATINKYATFMKSIHQADPLTKCYGIMPLPNTLTPKYLTVTLDDSSLK 84
QY 62 ITTLMRLRNLYVMGYSDPFNGNKCRIYHENDIT-STERDVENTLCSSSSRVAMSIN 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 ITTLMKRNLYVMGYADTYNG-KCRYHIFKDISWTERNDVMTLCPNPSRVCNKINLY 143
QY 121 NSLYPTMEKKAVERNNOVOIGIOLSSDICKISVDSPFKTEFFLLVAIOMVSEAR 180
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 DSSPALEKKGW-RPRSOVQIGIOLNSGIRKYGVDSTETKTEAEFLVAIOMVSEAR 202
QY 181 FKYLENOYKTNFNRAFYDPKVINLEEKMGKISEAHNAKNALPKPLEVDAKETKMIY 240
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 FKYLENOYKTNFNRAFYNAVLNLEESMGKISTRIHNAKNALTSPLLEKNANSGKMIY 262
QY 241 LRVDINRDVALLVYNGTCQT 263
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 LRVDIEPDVGLLKYNGTCQT 285

RESULT 4
RIP2_PHYAM STANDARD: PRT: 310 AA.
ID RIP2_PHYAM 040772:
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein 2 precursor (PAP-II) (Ribosome-inactivating protein)
DE (rRNA N-glycosidase) (EC 3.2.2.22).
GN PAP2 OR PAPII.
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=94307398; PubMed=6034016;
RA Poyet J.-L., Radom J., Hoeveiler A.;
RT "Isolation and characterization of a cDNA clone encoding the pokeweed
RT antiviral protein II from Phytolacca americana and its expression in
RT E. coli."
RL FEBS Lett. 347:268-272(1994).
RN [2]
RP SEQUENCE OF 26-55.
RC TISSUE=Leaf;
RX MEDLINE=65023392; PubMed=6091760;
RA Bjorn M.J., Larrick J., Platak M., Wilson K.J.;
RT "Characterization of translational inhibitors from Phytolacca
RT americana. Amino-terminal sequence determination and antibody-
RT inhibitor conjugates."
RL Biochim. Biophys. Acta 790:154-163(1984).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS. INHIBITS PROTEIN
CC SYNTHESIS IN BOTH PROKARYOTES AND EUKARYOTES.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LATE SUMMER LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PROGRESSIVELY WITH THE AGING OF THE
CC PLANT.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X78628; CAA55342.1;
CC HSSP: Q03464; IAPA.
CC InterPro: IPR001574; RIP.

```

```

DR Pfam: PF00161; RIP; 1.
DR PRINTS: PRO0396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN_1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW toxin; Signal.
FT SIGNAL 1 25
FT CHAIN 26 ? ANTIVIRAL PROTEIN 2.
FT PROPEP ? 310
FT ACT_SITE 197 197 BY SIMILARITY.
FT DISULFID 57 284 BY SIMILARITY.
FT DISULFID 106 123 BY SIMILARITY.
SQ SEQUENCE 310 AA; 34694 MW; 4D3BB001D7259D9F CRC64;

Query Match 33.4%; Score 453; DB 1; Length 310;
Best Local Similarity 41.0%; Pred. No. 3.4e-30;
Matches 112; Conservative 41; Mismatches 94; Indels 26; Gaps 11;

QY 3 NTTFDGNATINKYATFMESLRNQADPKIKCYGIMPLPNTSTPYLLVTKOGANLKT 62
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 SNIVEDYENATPEYNSNLTSLREAVNDKRLTCHGMATTLTEOPKRYVLVDLKFCS-GT 83
QY 63 ITTLMRLRNLYVMGYSDPFNGNKCRIYHENDIT-STERDVENTLCSSSSRVAMSIN 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 FTLAIRRGNTLLEGSIDYNG-KCRYHIFKD-----SSDAQETVCPGDKSKPGTNNIPY 138
QY 121 NSLYPTMEKKAVERNNOVOIGIOLSSDICKISVDSFP-----VKTEAFLLVAIOMVS 176
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 EKSKTGESK--GARKLGLGKITLSRMCKITGKATDOKOYOKNEAFLLVAIOMVT 196
QY 177 EAFKYLENOYKTNFNRA--FYDPKVINLEEKMGKISEAHNAKNAG-----ALPKPE 229
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 197 EASFKEKYNKVKAFPDANGYDPDAISLEKMDVSKEYI--AKYGTSGDSIVTLPGD 254
QY 230 LVDAKGRKIYLRVDINRDV-ALLKYNGTCQ 261
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 LKDENNKPMWTATMNDLKNIMALLTHV--TKK 285

RESULT 5
RIP6_SAPOF STANDARD: PRT: 299 AA.
ID RIP6_SAPOF 041392:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-6 precursor (SAP-6) (SO-6)
DE (rRNA N-glycosidase) (EC 3.2.2.22).
GN SAP6.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
RP SEQUENCE OF 1-283 FROM N.A., AND SEQUENCE OF 25-115; 206-213 AND
RP 234-277.
RC TISSUE=Leaf;
RX MEDLINE=89338421; PubMed=2547612;
RA Benatti L., Saccardo M.B., Dani M., Nitli G., Sassano M.,
RA Lorenzetti R., Lappi D.A., Soria M.;
RT "Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-
RT inactivating protein from Saponaria officinalis."
RL Eur. J. Biochem. 183:465-470(1989).
RN [2]
RP SEQUENCE OF 25-277 FROM N.A.
RX MEDLINE=93203250; PubMed=8454624;
RA Bartelemy I., Martineau D., Ong M., Matsunami R., Ling N.,
RA Benatti L., Cavallaro U., Soria M., Lappi D.A.;
RT "The expression of saporin, a ribosome-inactivating protein from the
RT plant Saponaria officinalis, in Escherichia coli."
RL Eur. J. Biol. Chem. 268:6541-6548(1993).
RN [3]
RP SEQUENCE OF 275-299 FROM N.A.

```



```

RC TISSUE-Leaf.
RX MEDLINE=92038053; PubMed=1936274;
RA Benatti L., Nitli G., Solinas M., Valsasina B., Vitale A.,
RA Ceriotti A., Soria M.R.;
RT "A Saporin-6 cDNA containing a precursor sequence coding for a
RT carboxyl-terminal extension.";
RL FEBS Lett. 291:285-286(1991).
RN [4]
RP SEQUENCE OF 25-72 AND 114-154.
RX MEDLINE=90220515; PubMed=2325629;
RA Fordham-Skelton A.P., Yarwood A., Croy R.R.D.;
RT "Synthesis of saporin gene probes from partial protein sequence data:
RT use of inosine-oligonucleotides, genomic DNA and the polymerase chain
RT reaction.";
RL Mol. Genet. 221:134-138(1990).
CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR
CC PHARMACOLOGICAL APPLICATIONS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- TISSUE SPECIFICITY: SEEDS AND LEAVES OF THE PLANT.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X15655; CAA33685.1; -
DR EMBL: S57638; AAB25863.1; -
DR EMBL: X69133; CAA48889.1; -
DR EMBL: X64917; CAA46110.1; -
DR EMBL: A00352; CAA00055.1; -
DR PIR: S05205; S05205.
DR HSSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PRO0396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; signal;
KW Multigene family.
FT CHAIN 1 24
FT SIGNAL 1 24
FT PROPEP 25 277
FT ACT_SITE 278 299
FT CARBOHYD 200 200
FT VARIANT 283 283
FT VARIANT 72 72
FT VARIANT 115 115
FT CONFLICT 123 123
FT CONFLICT 212 212
SQ SEQUENCE 299 AA; 33607 MW; 4BC312958BB4E79B CRC64;

Query Match 25.2%; Score 342; DB 1; Length 299;
Best Local Similarity 35.9%; Pred. No. 4.5e-21;
Matches 94; Conservative 51; Mismatches 97; Indels 20; Caps 9;

OY 2 INTITDAGNATINKATPESLRNOAKDPKLCYGPMLPTNSTPKYLKLOGANL 60
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 25 VTSITDLVNPPTAGQSSFYDKIRNNVKDNLKYGTDIAVICPPSKKFLRINPQSSR- 83
OY 61 KTTTLMRRNNLVYMGSDPFNGNCKR-YHIFNDITSTERTDVENTLCSSSSRVAMSN 119
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 84 GTVSLGLKRDNLVYAVYLAAMDNTNVRAYFRSEITSSEST---ALFPETATNOKALE 139
OY 120 YNSLYPTMEKKAEEV---NSRNOVOIGIOLSSDICKSGVDSFPVKTAEFLVLAIQMW 175
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 140 YTEDYOSIEKNAQITOGDOKSKELGIDLLTSMBAVN-KKARVVKDEARFLIAIQMT 198
OY 176 SEARAFKIENOVKTNENRAFPDPKVINLEEKWGKISEAIIH-NAKNGALPKPLELVDAR 234

```

```

DB 199 AEAARFRYIOLNLIKRPKNFSENKVIQFEVNMKKRISTAIYGDANKNGVFNKDYGDFGK 258
OY 235 GTKWIVLRDEINRDVALLKVV 256
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 259 -----VRQVKDL--QMGLLMTL 273

RESULT 6
RIPS_SAPOF
ID RIPS_SAPOF STANDARD; PRT; 253 AA.
AC Q41869;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-5 (EC 3.2.2.22) (SAP-5) (tRNA N-
DE glycosidase).
GN SAP5.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Leaf.
RX MEDLINE=93203250; PubMed=8454624;
RA Barthelmy I., Martineau D., Ong M., Matsunami R., Ling N.,
RA Benatti L., Cavallaro U., Soria M., Lappi D.A.;
RT "The expression of saporin, a ribosome-inactivating protein from the
RT plant Saponaria officinalis, in Escherichia coli.";
RL J. Biol. Chem. 268:6541-6548(1993).
CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X69131; CAA48885.1; -
DR EMBL: X69132; CAA48886.1; -
DR HSSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PROSITE: PS00275; SHIGA_RICIN.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW Multigene family.
FT ACT_SITE 176 176
SQ SEQUENCE 253 AA; 28556 MW; 5369693E13D0F594D CRC64;

Query Match 24.8%; Score 337; DB 1; Length 253;
Best Local Similarity 35.5%; Pred. No. 9.3e-21;
Matches 93; Conservative 50; Mismatches 99; Indels 20; Caps 9;

OY 2 INTITDAGNATINKATPESLRNOAKDPKLCYGPMLPTNSTPKYLKLOGANL 60
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 VTSITDLVNPPTAGQSSFYDKIRNNVKDNLKYGTDIAVICPPSKKFLRINPQSSR- 59
OY 61 KTTTLMRRNNLVYMGSDPFNGNCKR-YHIFNDITSTERTDVENTLCSSSSRVAMSN 119
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 60 GTVSLGLKRDNLVYAVYLAAMDNTNVRAYFRSEITSSEST---ALFPETATNOKALE 115
OY 120 YNSLYPTMEKKAEEV---NSRNOVOIGIOLSSDICKSGVDSFPVKTAEFLVLAIQMW 175
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 116 YTEDYOSIEKNAQITOGDOKSKELGIDLLTSMBAVN-KKARVVKDEARFLIAIQMT 174

```

Db	116	TTEDYQSIEKNAQNIQSGSKSRKDELGLDILLTISHENAVN-KKARVYKNEARFLIAIQMT	174
Oy	176	SEAAEFKIEIENOVKTENFRAPYPPDRKVINLEEKMKWCKISEAIIH-NAKNGALPKPLELVYAK	234
Db	175	AEAAFRFYIQLVLVINFPENKENSEKNIQIOFEVNMKKIISATYIGDAKNGVFNKDYDPGFCG	234
Oy	235	GTKWIVLRVDEINRDVALTKYV	256
Db	235	-----VROVKDL--OMGLMLYL	249

  

RESULT 8			
ID	RIIP2_SAPOF	STANDARD:	PRT: 292 AA.
AC	P27559; Q9SAP5; Q41390;		
DT	01-AUG-1992 (Rel. 23, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Ribosome-inactivating protein.Saporin-2 precursor (SAP-2) (SO-2)		
DE	(rRNA N-glycosidase) (EC 3.2.2.22).		
GN	SAP2.		
OS	Saponaria officinalis (Common soapwort).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.		
OX	NCBI_TaxID=3572;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92049247; PubMed=1719367;		
RA	Fordham-Stelton A.P., Taylor P.E., Hartley M.R., Croy R.R.D.;		
RT	"Characterisation of saporin genes: in vitro expression and ribosome		
RT	inactivation.";		
RL	Mol. Gen. Genet. 229:460-466(1991).		
RN	[2]		
RP	SEQUENCE OF 25-284 FROM N.A.		
RC	TISSUE-Leaf;		
RX	MEDLINE=93203250; PubMed=8454624;		
RA	Barthelemy I., Martineau D., Ong M., Matsunami R., Ling N.,		
RA	Benatti L., Cavallaro U., Sorita M., Lappi D.A.;		
RT	"The expression of saporin, a ribosome-inactivating protein from the		
RT	plant Saponaria officinalis, in Escherichia coli.";		
RL	J. Biol. Chem. 268:6541-6548(1993).		
CC	-1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS		
CC	PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR		
CC	PHARMACOLOGICAL APPLICATIONS.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one		
CC	specific adenosine on the 28S rRNA.		
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
CC	TYPE 1 RIP SUBFAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ,		
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
DR	EMBL: X59255; CAA41948.1; -		
DR	EMBL: X69132; CAA48886.1; -		
DR	EMBL: X69133; CAA48887.1; -		
DR	PIR: S17933; RLOHG2.		
DR	HSSP: P10297; ICGG.		
DR	InterPro: IPR001574; RIP.		
DR	Pfam: PF00161; RIP.1.		
DR	PRINTS: PR00396; SHIGARICIN.		
DR	ProSITE: PS00275; SHIGARICIN.1.		
KM	Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;		
KM	Multigene family.		
FT	SIGNAL	1	24
FT	CHAIN	25	292
FT	ACT SITE	200	200
FT	VARIANT	72	72
FT			D -> E.
FT			BY SIMILARITY.
FT			RIBOSOME-INACTIVATING PROTEIN SAPORIN-2.

```

RESULT 9
RIP0_DIACA      STANDARD:      PRT:      293 AA.
AC      RIP0_DIACA      P24476;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Antiviral protein DAP-30 precursor (Ribosome-inactivating protein)
OS      (rRNA N-glycosidase) (EC 3.2.2.22) (Dianthin 30).
OC      Dianthus caryophyllus (Carnation) (Clove pink).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;
OC      Caryophyllales; Caryophyllaceae; Dianthus.
OX      NCBI_TaxId=3570;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91355219; PubMed=1840496;
RA      Legname G., Bellosta P., Gromo G., Modena D., Keen J.N., Roberts L.M.,
RA      Lord J.M.;
RT      "Nucleotide sequence of cDNA coding for dianthin 30, a ribosome
RL      inactivating protein from Dianthus caryophyllus.";
RN      Blochim. Biophys. Acta 1090:119-122(1991).
RN      [2]
RP      SEQUENCE OF 24-82.
RC      TISSUE=leaf;
RX      MEDLINE=92037998; PubMed=1936243;
RA      Lee-Huang S., Kung H.-F., Huang P.L., Huang P.L., Li B.-Q., Huang P.,
RA      Huang H.L., Chen H.-C.;
RT      "A new class of anti-HIV agents: GAP31, DAPS 30 and 32.";
RL      FEBS Lett. 291:139-144(1991).
CC      -I- FUNCTION: SINGLE-CHAIN RIBOSOME-INACTIVATING PROTEIN, POSSESSING
CC      HIGH ANTIVIRAL POTENCY AND LOW TOXICITY TO NORMAL CELLS IN CULTURE
CC      AND TO INTACT ANIMALS. CAPABLE OF INHIBITING HIV-1 INFECTION AND
CC      REPLICATION.
CC      -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC      TYPE 1 RIP SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboratio
CC      between the Swiss institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics institute. There are no restrictions on it
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercia
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce
CC      or send an email to license@isb-sib.ch).

```

CC EMBL: X59260: CAA41953.1: ALU\_SEQ.  
DR PIR: S17519; S17519.  
DR HSSP: Q03464; IAPA.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP; 1.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolyase;  
KW Toxin; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 293 ANTI-VIRAL PROTEIN DAP--30.  
FT ACT\_SITE 200 200 BY SIMILARITY.  
SQ SEQUENCE 293 AA: 32717 MW: AC65AAC872504F2 CRC64;  
  
Query Match 23.5%; Score 319.5; DB 1; Length 293;  
Best Local Similarity 35.1%; Pred. No. 3; 1e-19;  
Matches 92; Conservative 47; Mismatches 96; Indels 27; Gaps 11  
  
QY 6 TFDAGNATITNKATMTMESLRNOKDPKLCYCG---IPMLPDINSTRKYLVLKIQGNLTK 62  
DB 28 TLNLNPNPSQSYSSFLDQIRNNVRDSTL-IGCTDVAIVGASPTDKFLRLNGPR-GT 85  
QY 63 ITLMRLRNLLYMGVSDPFGNKCR-YHIFNDITSPERDVENTLCSSSRVAMSJNY 121  
DB 86 VSLGRKRELLYVAIILAMNANVRYYIRKNOITTSSELTALPFEVVAADK---LEIG 141  
QY 122 SLPTMEKKAEEV---NSRNQYLGILSDIGKISGVDS--FPVKTEAFFLLVAIOMV 175  
DB 142 EDYQAIENKAKITTGQDSRKEGLGGINLL---ITMIDGVNKKRVYVVKDEARFLIAIOMT 198  
QY 176 SEAAAFKTIENOVKTNFNRAFPDPKRVINLBEKMKGISPAIH-NAKNGAI-PKLELYDAK 234  
DB 199 AEAARFYRIQNTLVNFKFNPKFDPSEKNVIOFOVSWSKISTAFIDCKNGVFNKDYDFGFGK 258  
QY 235 GKKWIVLRVDEINRDVALIKYV 256  
DB 259 -----VRQAKDL--QWGLLKYL 273  
  
RESULT 10  
RIPC\_GELMU  
ID RIPC\_GELMU STANDARD: PRT; 316 AA.  
AC P3186;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein gelonin precursor (rRNA N-glycosidase)  
DE (EC 3.2.2.22).  
OS Gelonium multiflorum (Euphorbiaceae himalaya).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Malpighiales; Euphorbiaceae; Gelonium.  
OX NCBI\_TaxID=3979;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94085781; PubMed=7916721;  
RA Nolan P.A., Garrison D.A., Beller M.;  
RT "Cloning and expression of a gene encoding gelonin, a ribosome-  
inactivating protein from Gelonium multiflorum.";  
RL Gene 134:223-227(1993).  
RN (2)  
RP SEQUENCE OF 47-93.  
RC TISSUE=Seed;  
RX MEDLINE=89326691; PubMed=2753596;  
RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Scirpe F., Soria M.,  
RA Lapi D.;  
RT "N-terminal sequence of some ribosome-inactivating proteins.";  
RL Int. J. Pept. Protein Res. 33:263-267(1989).  
RN (3)  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
RX MEDLINE=95333189; PubMed=7608981;

RA Hosur M.V., Nair B., Satyamurthy P., Misquith S., Suroolia A.,  
RA Kannan K.K.;  
RT "X-ray structure of gelonin at 1.8-A resolution.";  
RL J. Mol. Biol. 250:368-380(1995).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.  
CC -----  
CC This SWISS-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>  
CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
CC -----  
DR EMBL: L12243; AAA16312.1;  
DR PIR: S16489; S16489.  
DR HSSP: P09889; 1MRJ.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP. 1.  
DR PRINTS: PR00386; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA-RICIN; FALSE\_NEG.  
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;  
KW Glycoprotein.  
FT SIGNAL 1 26  
FT PROPEP 27 46 POTENTIAL.  
FT CHAIN 47 237 RIBOSOME-INACTIVATING PROTEIN GELONIN.  
FT PROPEP 298 316 MISSING IN MATURE PROTEIN.  
FT DISULFID 90 96  
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .).  
FT ACT\_SITE 212 212  
FT CONFLICT 90 90  
FT CONFLICT 93 93 C -> K (IN REF. 2).  
FT CONFLICT 93 93 P -> D (IN REF. 2).  
SQ SEQUENCE 316 AA: 35418 MW: 1252FE3E710901B85 CRC64:  
Query Match 23.1%; Score 313; DB 1; Length 316;  
Best Local Similarity 32.1%; Pred No. 1.2e-18;  
Matches 86; Conservative 50; Mismatches 110; Indels 22; Gaps 8;  
OY 2 INTTFDAGNATINKYATFMESLRNQADPKLKCXGIMLPDPTNTPK--YLVKLOGAN 59  
DB 48 LDTVSFSTKATYTYVNFNLRLRYKLRK-PGNSNGIGILRRKODPKCFVLVALSDN 106  
OY 60 LKTTLMRLRNRLLYMGYSDDPNKCKRHIFNDITERTDV-ENTLCSSSSSRVAMSI 118  
DB 107 GGLAEIADVTSVYVVGQ----VRNRSYFFKADPAAYEGLFKNT-----IKTRL 153  
OY 119 NNSLYPTMEKKAENVSRNOVLOGIOLSDIGK--SGVDSFPVKTEAFILVALIOWVS 176  
DB 154 HGGGSYPSLE--GEAYRETTDLGLEPLRIGIKKIDEVAIDWKYDPTETIASLLVLIOWVS 211  
OY 177 EAARPKYIENOVKTNFNRAFYPPDKVINLEEKMGKISEAIIH-NAKNGALPKPLELVDAKG 235  
DB 212 EAARPTFIENQIRNRFQORIRPANNITILENKKMGKLSLOITSGANGFSEAVELERANG 271  
OY 236 TKMYLVRLDEINRQVALLKYNGCQTT 263  
DB 272 KKYYTAVDOVKPKIALLKLVDPDKPKTS 299

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:  
OC eucosids I: Malpighiales: Euphorbiaceae: Ricinus.  
OX NCBI\_TaxID=3988;  
RN (1)  
RN SEQUENCE FROM N.A.  
RX MEDLINE=86067214; PubMed=2999712;  
RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,  
RA Weaver R.F.;  
RT "Genomic cloning and characterization of a ricin gene from Ricinus  
RT communis.";  
RL Nucleic Acids Res. 13:8019-8033(1985).  
RN (2)  
RN SEQUENCE FROM N.A.  
RX MEDLINE=92163016; PubMed=1371405;  
RA Tregear J.W., Roberts L.M.;  
RT "The lectin gene family of Ricinus communis: cloning of a functional  
RT ricin gene and three lectin pseudogenes.";  
RL Plant Mol. Biol. 18:515-525(1992).  
RN (3)  
RN SEQUENCE OF 12-576 FROM N.A.  
RX MEDLINE=85179479; PubMed=3838723;  
RA Lamb A., Roberts L.M., Lord J.M.;  
RT "Nucleotide sequence of cloned cDNA coding for preproricin.";  
RL Eur. J. Biochem. 148:265-270(1985).  
RN (4)  
RN SEQUENCE OF 36-302.  
RA Yoshitake S., Funatsu G., Funatsu M.;  
RT "Isolation and sequences of peptic peptides, and the complete  
RT sequence of the chain of ricin-D.";  
RL Agric. Biol. Chem. 42:1267-1274(1978).  
RN (5)  
RN SEQUENCE OF 315-576.  
RA Funatsu G., Kimura M., Funatsu M.;  
RT "Primary structure of Ala chain of ricin D.";  
RL Agric. Biol. Chem. 43:2221-2224(1979).  
RN (6)  
RN CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.  
RX MEDLINE=90344223; PubMed=1368517;  
RA Kimura Y., Kusunoku H., Tada M., Takagi S., Funatsu G.;  
RT "Structural analyses of sugar chains from ricin A-chain variant.";  
RL Agric. Biol. Chem. 54:157-162(1990).  
RN (7)  
RN REVIEW  
RX MEDLINE=21480122; PubMed=11595634;  
RA Olsnes S., Kozlov J.V.;  
RT "Ricin.";  
RL Toxicon 39:1723-1728(2001).  
RN (8)  
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RX MEDLINE=87165983; PubMed=3558397;  
RA Monfort W., Villafraza J.E., Monzinger A.F., Ernst S.R., Katzin B.,  
RA Rutenber E., Xuong N.H., Hamlin R., Roberts J.D.;  
RT "The three-dimensional structure of ricin at 2.8 A.";  
RL J. Biol. Chem. 262:5398-5403(1987).  
RN (9)  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
RX MEDLINE=91352004; PubMed=1881881;  
RA Katzin B.J., Collins E.J., Roberts J.D.;  
RT "Structure of ricin A-chain at 2.5 A.";  
RL Proteins 10:251-259(1991).  
RN (10)  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.  
RX MEDLINE=91352005; PubMed=1881882;  
RA Rutenber E., Roberts J.D.;  
RT "Structure of ricin B-chain at 2.5-A resolution.";  
RL Proteins 10:260-269(1991).  
RN (11)  
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.  
RX MEDLINE=95082010; PubMed=7990130;  
RA Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,  
RA Pauplit R.A.;  
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";

RL J. Mol. Biol. 244:410-422(1994).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.  
 RX MEDLINE:96374222; PubMed:8780513;  
 RA Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,  
 RT Molina-Svith M.C., Robertus J.D.;  
 RA "Structure and activity of an active site substitution of ricin A  
 RT chain."  
 RL Biochemistry 35:11098-11103(1996).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE:97240820; PubMed:9086280;  
 RA Yan X., Hollis T., Svith M., Day P., Monzingo A.F., Milne G.W.,  
 RT Robertus J.D.;  
 RA "Structure-based identification of a ricin inhibitor."  
 RL J. Mol. Biol. 266:1043-1049(1997).  
 RN [14]  
 RP MUTAGENESIS.  
 RX MEDLINE:93165612; PubMed:1287657;  
 RA Kin Y., Robertus J.D.;  
 RT "Analysis of several key active site residues of ricin A chain by  
 RT mutagenesis and X-ray crystallography."  
 RL Protein Eng. 5:775-779(1992).  
 CC -1- FUNCTION: Ricin is highly toxic to animal cells and to a less  
 CC extent to plant cells. The A chain is responsible for inhibiting  
 CC protein synthesis through the catalytic inactivation of 60S  
 CC ribosomal subunits. It acts as a glycosidase that removes a  
 CC specific adenine residue from an exposed loop of 28S ribosomal  
 CC RNA. As this loop is involved in the binding of elongation  
 CC factors, the modified ribosomes are unable to support protein  
 CC synthesis. The A chain can inactivate a few thousand ribosomes  
 CC per minute, thus inactivating them faster than the cell can make  
 CC new ones. A single A-chain molecule can therefore kill an animal  
 CC cell. The B chain binds to cell receptors and facilitates the  
 CC entry into the cell of the A chain. B chains are also responsible  
 CC for cell agglutination (lectin activity). It binds to beta-D-  
 CC galactopyranoside moieties.  
 CC CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -1- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE  
 CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.  
 CC CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS  
 CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X01179; CA26939.1; -  
 DR EMBL: X52908; CAA37095.1; -  
 DR EMBL: X02388; CAA26230.1; -  
 DR EMBL: A12892; CAA01058.1; -  
 DR PIR: A24041; RLCSD.  
 DR PDB: 2AAT; 31-JAN-94.  
 DR PDB: 1APG; 31-JAN-94.  
 DR PDB: 1FMP; 31-OCT-93.  
 DR PDB: 1IFS; 14-JAN-98.  
 DR PDB: 1IFU; 14-JAN-98.  
 DR PDB: 1IRC; 31-OCT-93.  
 DR PDB: 1OBS; 16-JUN-97.  
 DR PDB: 1OBT; 16-JUN-97.  
 DR PDB: 1BR5; 02-SEP-98.

DR PDB: 1BR6; 02-SEP-98.  
 DR GlycosylatedB: P02879; -  
 DR InterPro: IPR001574; RIP.  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR Pfam: PF00161; RIP; 1.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR SMART: SM00458; RICIN; 2.  
 DR PROSITE: PS50231; RICIN\_B\_LLECTIN; 2.  
 DR PROSITE: PS00275; SHIGA; RICIN; 1.  
 DR Plant defense: Hydrolase: Protein synthesis inhibitor; Toxin; Repeat;  
 KW Glycoprotein; Lectin; Signal; 3D-structure.  
 FT SIGNAL 1 35  
 FT CHAIN 36 302  
 FT PEPTIDE 303 314  
 FT CHAIN 315 576  
 FT DOMAIN 321 448  
 FT DOMAIN 451 575  
 FT REPEAT 331 373  
 FT REPEAT 374 414  
 FT REPEAT 417 449  
 FT REPEAT 462 497  
 FT REPEAT 501 540  
 FT REPEAT 543 570  
 FT ACT\_SITE 212 212  
 FT DISULFID 294 318  
 FT DISULFID 334 353  
 FT DISULFID 377 394  
 FT DISULFID 465 478  
 FT DISULFID 504 521  
 FT CARBOHYD 45 45  
 FT CARBOHYD 271 271  
 FT CARBOHYD 409 409  
 FT CARBOHYD 449 449  
 FT CONFLICT 76 76  
 FT CONFLICT 551 551  
 FT STRAND 43 47  
 FT STRAND 49 50  
 FT TURN 50 67  
 FT HELIX 53 73  
 FT STRAND 73 74  
 FT TURN 75 76  
 FT STRAND 77 77  
 FT TURN 88 90  
 N-LINKED (GLCNAC. . .)  
 /FTID-CAR.000080.  
 /N-LINKED (GLCNAC. . .): IN MINOR A-CHAIN  
 VARIANT.  
 /FTID-CAR.000081.  
 /N-LINKED (GLCNAC. . .)  
 N-LINKED (GLCNAC. . .)  
 E -> D (IN REF. 3).  
 A -> R (IN REF. 3).  
 INTERCHAIN.  
 Query Match 21.4%; Score 291; DB 1; Length 576;  
 Best Local Similarity 30.4%; Pred. No. 1; 7e-16;  
 Matches 83; Conservative 44; Mismatches 100; Indels 46; Gaps 10;  
 QY 5 ITFDAGNATINKYATFMESLRNOAKDPKLCYGPMLPTNSTP---KYLVLKAGANLK 61  
 DB 44 INTTGTGATVOSTNTNIRAVRGTLTGADVRHEIPVLPNRVGLPIORLIVELSHAEU 103  
 QY 62 TITLMLRRNLVYMGYSDFPENGKCRV-----HIFNDITSTERPDVENTYICS 108  
 DB 104 SVTLALDVTNAVYVGR---AGNSAVFFPHDNOEDAEATHLF-----TDVON----- 148  
 QY 109 SSSSRVAMSINYSLSLPTMEKKEVSRNOVOIGITLSSDICKI-----SGVDSRPVKTE 164  
 DB 149 ---RYTFAGFGN--YDRLEQLAG-NIRENIELGNPLLEAIALYYSSTGTOTLPTLAR 201  
 QY 165 AFFLLVAIQWVSEAREFYENOVKT--NFNRAFYDPKVINLEEKMGKISEAIIHNAKNG 222  
 DB 202 SF--IICIQMISAAAFQYIEGMRIRIRINRSASDPVITLLENSMGRSLTAIOESNOC 259  
 QY 223 ALKPPLDYDAKGTKMIIVLVEIDINRDVALKY 255  
 DB 260 AFASPIQLORRNGSKFSYDVSTILPIIALMVY 292

RESULT 12

RIP1-TRIAN STANDARD: PRT: 294 AA.

AC P56626; 092077.

DT 15-DEC-1998 (Rel. 37, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Type I ribosome-inactivating protein trichoangulina precursor (rRNA N-glycosidase) (EC 3.2.2.22) (RIP) (Trichoangulin).

GN TCA.

OS Trichosanthes anguina (Snake gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.

OX NCBI\_TaxID=50544;

RN [1]

RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.

RC STRAIN=cv. Anguina; TISSUE=Seed;

RC MEDLINE=99132006; PubMed=991318;

RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H., Lin J.-Y.;

RT "Purification, characterization and molecular cloning of trichoangulin, a novel type I ribosome-inactivating protein from the seeds of Trichosanthes anguina."

RT Biochem. J. 338:211-219(1999).

RL [2]

RN SEQUENCE OF 20-264.

RC TISSUE=Seed;

RA Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;

RT "Amino acid sequence of trichoangulina, a ribosomal-inactivating protein from Trichosanthes anguina seeds."

RT J. Biomed. Sci. 3:178-186(1996).

CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN RIBOSOMES.

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE I RIP SUBFAMILY.

CC [1]

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

CC EMBL: AF055086; AAD02686.1; -

CC HSSP: P33185; 1BRV.

CC InterPro: IPR001574; RIP.

CC Pfam: PF00161; RIP.1.

CC PRINTS: PR00396; SHIGARICIN.

CC PROSITE: PS00275; SHIGA\_RICIN; FALSE\_NEG.

CC KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;

CC GLYCOPROTEIN; Signal.

CC SIGNAL 1 19

CC CHAIN 20 264

CC TYPE I RIBOSOME-INACTIVATING PROTEIN

CC TRICHOANGULINA.

CC PROPEP 265 294

CC ACT\_SITE 177 177

CC ACT\_SITE 180 180

CC CARBOHYD 70 70

CC CARBOHYD 220 220

CC CONFLICT 51 31

CC CONFLICT 65 65

CC CONFLICT 84 84

CC CONFLICT 152 152

CC CONFLICT 174 174

CC CONFLICT 245 245

CC SEQUENCE 294 AA; 32234 MW; DA4F8B7CE3290994 CRC64;

Query Match 21.2%; Score 287.5; DB 1; Length 294;

Best Local Similarity 30.7%; Pred. No. 1,3e-16;

Matches 80; Conservative 52; Mismatches 104; Indels 25; Gaps 9;

QY 2 INTITPDAGNATINKYATFMEESLRNQAOKPKICGIPMLPDTNSTPKYL-LVKIUGANL 60

DB 18 IDVSEDDSTAKKSSSTFTQLRALPTQGTVC-GIPLLPSTAGSOMFRFFNLTVNYND 76

QY 61 KTTITLRRNNLYVGVY-SDPENGKCKRHHFNDDITSPERTVENTLSSSSSRAMSTN 119

DB 77 ETVVAVNVNTNVIYIAYRADAVS-----YFFED---TPAEAFKILFAGTKVLPYSGN 127

QY 120 YNSLYPTHEKKAENVSRNOVLGIOLSSD)GKISGVDSFPYKTEAFPLIYAIQVSEAA 179

DB 128 YDKLOSIVVGKQ-----RDMIEIGIPALSS---AITNMVYDYQSTAAALLVLIQCTAAEA 179

QY 180 RFKYIENGVKTNFNAFYDPDPKVIYLEEKMKGISALINAK---NGALPKPLEYDANKT 236

DB 180 RKYIEQOVSSHISNFPYQNAVLSLENKKWALSQIOIANRTGHPENVEYELNPDCT 239

QY 237 KWIYLRVDE--INRDVALKY 255

DB 240 RESVNTSAGVYKGNIKLLY 260

RESULT 13

RIP3\_SAPOF

ID RIP3\_SAPOF STANDARD: PRT: 236 AA.

AC P27560;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein saporin-3 (SAP-3) (SO-3) (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).

GN SAP3.

OS Saponaria officinalis (Common soapwort).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Saponaria.

OX NCBI\_TaxID=3572;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=92049247; PubMed=1719367;

RA Fordham-Skelton A.P., Taylor P.E., Hartley M.R., Croy R.R.D.;

RT "Characterisation of saporin genes: in vitro expression and ribosome inactivation."

RT Mol. Gen. Genet. 229:460-466(1991).

CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR PHARMACOLOGICAL APPLICATIONS.

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE I RIP SUBFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: X59256; CAA41949.1; -

CC PIR: S17932; S17932.

CC HSSP: P10297; 1OCG.

CC InterPro: IPR001574; RIP.

CC Pfam: PF00161; RIP.1.

CC PROSITE: PS00275; SHIGA\_RICIN; 1.

CC KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;

CC MULTIGENE FAMILY.

CC NON\_TER 1 1

CC ACT\_SITE 148 148

CC SEQUENCE 236 AA; 26591 MW; DE3D68BA50FC054 CRC64;

Query Match 20.9%; Score 283; DB 1; Length 236;

Best Local Similarity 35.8%; Pred. No. 2.4e-16;  
Matches 86; Conservative 41; Mismatches 87; Indels 26; Gaps 10;

QY 30 DKLKCYSIPM-LPTDINSFKYLLKLOGANLKTITLMRRNNLYVMGSDPFNGKCR- 87  
DB 1 DNLKYGTDIVICPPSRDKFLRLPFOSSR-GTVSLGKRLNLYVALAMDANVNNA 59  
OY 88 YHIFNDITSTERTDVENTLCCSSSSRVAMSYNSLYPTMEKRAEV---NSRNOVOLGI 143  
DB 60 YFGEFTTISAELT---TLPEATVANOKALEYEDYOSIEKNKITEGDKTRKELGLOI 115  
OY 144 QILSS---DIGKISGVDPVTEAFELLVAIQWSEARFYIENQVKTNNRAFPDP 200  
DB 116 NLSTLMDAVNKKARV---VKNEARFLIAIQMTAEARFYIQNLVTKNPNKFNSED 171  
OY 201 KYINLEEKWKISEAH-NAKNGALPKPELVDACTKIVILRVDEINDVALLKYVNT 259  
DB 172 KVIQFOVNSKISKALYGDANKGVENKDYFGFGK---VRQVQDL--QMGLLMYLGT 224

RESULT 14  
AGCL\_RICCO STANDARD: PRT: 564 AA.

AC P06750;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Agglutinin precursor (RCM) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].  
OS Ricinus communis (Castor bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
OX NCBI\_TaxID=3988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86059449; PubMed=2999130;  
RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;  
RT "The primary sequence of Ricinus communis agglutinin. Comparison with Ricin.";  
RL J. Biol. Chem. 260:15682-15686(1985).  
RN [2]  
RP SEQUENCE OF 303-564.  
RC TISSUE=Seed.  
RA Araki T., Yoshioke Y., Funatsu G.;  
RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds.";  
RL Biochim. Biophys. Acta 872:277-285(1986).  
RN [3]  
RP SEQUENCE OF 303-337.  
RX MEDLINE=80178723; PubMed=6768555;  
RA Lin T.T.-S., Li S.S.-L.;  
RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";  
RL Eur. J. Biochem. 105:453-459(1980).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M12089; AAA33869.1;  
DR EMBL: S40368; AAB22584.1;  
DR PIR: A24261; RLCSAG.  
DR HSSP: P02879; 1BR6.

DR GlycositedB: P06750; -.  
DR InterPro: IPR001574; RIP.  
DR InterPro: IPR000772; Ricin\_B\_lectin.  
DR Pfam: PF00161; RIP; 1.  
DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
DR PRINTS: PR00396; SHIGARICIN.  
DR SMART: SM00458; RICIN; 2.  
DR PROSITE: PS00231; RICIN\_B\_LECTIN; 2.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
KW Plant defense; Hydrolase; protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 290  
FT PROPEP 291 302  
FT CHAIN 303 564  
FT DOMAIN 309 436  
FT DOMAIN 439 563  
FT REPEAT 319 361  
FT REPEAT 362 402  
FT REPEAT 405 437  
FT REPEAT 450 485  
FT REPEAT 489 528  
FT REPEAT 531 558  
FT ACT\_SITE 200 200  
FT DISULFID 282 306  
FT DISULFID 322 341  
FT DISULFID 365 382  
FT DISULFID 453 466  
FT DISULFID 482 509  
FT CARBOHYD 34 34  
FT CARBOHYD 259 259  
FT CARBOHYD 397 397  
FT CARBOHYD 437 437  
FT CONFLICT 331 331  
FT CONFLICT 362 362  
FT CONFLICT 374 374  
FT CONFLICT 404 404  
FT CONFLICT 552 552  
SQ SEQUENCE 564 AA: 62851 MW: D455F2A72F609759 CRC64;

Query Match 20.0%; Score 271.5; DB 1; Length 564;  
Best Local Similarity 28.7%; Pred. No. 6.6e-15;  
Matches 77; Conservative 47; Mismatches 107; Indels 37; Gaps 7;

OY 5 IFPDAGNATINKYAFMSELSRQADPKKCGIPLPTNSTP---KYLKLOGANLX 61  
DB 33 INFTADATVESYTNFIRVRSHLTGTADVREHPIVLRVGLPLISQRTLVLSNHAEL 92  
OY 62 TITLMRLRNNLYVMG-----YSDPFNGKCRHIFNDITSTERTDVENTLCCSSS 111  
DB 93 SVTLALDVNNAVYVCGRAGNSAYFFHPDQDEAEATHLF-----TDVON----- 137  
OY 112 SRVAMSYNSLYPTMEKRAEVNSRNOVOLGIOLSSDIGKI--SCVDSFPVKTAFIL 169  
DB 138 ---SFTFAFGVNDRLQGLGCL--RENIELGCLPLEDAISALYYVSTGTOIPFLARSP 192  
OY 170 VALQWSEARFYIENQVKT--NFRARVPPPKYINLEEKWKISEAHNKNKALRPP 227  
DB 193 VCIQWSEARFYIENQVKT--NFRARVPPPKYINLEEKWKISEAHNKNKALRPP 252  
OY 228 LELVDAGTKWIVILRVDEINRDVALKY 255  
DB 253 IQLQRNSKSFNVYDSILIPILALMVY 280

RESULT 15  
RIP2\_BRYDI STANDARD: PRT: 282 AA.

AC P98184; O9S8J0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein bryodin II precursor (rRNA N-

```
DE glycosidase) (EC 3.2.2.22) (BD2).
OS Bryonia dioica (Red bryony).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OX NCBI_TaxID=3652;
RN [1]
RP SEQUENCE FROM N.A.
RA Siegall C.B., Gawlak S.L., Marguardt H.:
RT "Bryodin 2 a ribosome-inactivating protein isolated from the plant
RL Bryonia dioica."
RN Patient number US5597569, 28-JAN-1997.
RN [2]
RP SEQUENCE OF 22-42.
RC TISSUE=ROOT;
RX MEDLINE=95151812; PubMed=7849072;
RA Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
RA Marguardt H.;
RT "Characterization of ribosome-inactivating proteins isolated from
RT Bryonia dioica and their utility as carcinoma-reactive
RT immunokonjugates.";
RT Bioconj. Chem. 5:423-429(1994).
CC - FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE I, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
-----
CC EMBL: J34238; NOT_ANNOTATED_CDS.
DR HSSP: P09989; IMRJ.
DR InterPro: IPRO01574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
FT ACT_SITE 183 183 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GLCNAC...) (POTENTIAL).
SO SEQUENCE 282 AA; 30754 MW; C32BEFF6A873769C CRC64;

Query Match 19.2%; Score 260; DB 1; Length 282;
Best Local Similarity 31.4%; Pred. No. 2,3e-14;
Matches 80; Conservative 41; Mismatches 116; Indels 18; Gaps 7;
```

```
Db          250 NVNSPVVKGIALLLY 264

Search completed: July  2, 2003, 11:37:37
Job time : 12.338 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 19.022 Seconds

(without alignments)  
1329.163 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357

Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALLKVNGCTCOT 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1096.5	80.8	261	2 JF0401	antiviral protein
2	1050	77.4	313	2 S17757	RNA N-glycosidase
3	1014.5	74.8	294	2 S28421	RNA N-glycosidase
4	453	33.4	310	2 S46239	ribosome-inactivat
5	425.5	31.4	289	2 T12573	RNA N-glycosidase
6	394	29.0	272	2 JCA811	betavulgin - beet
7	343.5	25.3	253	2 A58923	RNA N-glycosidase
8	342	25.2	283	2 S05205	RNA N-glycosidase
9	341	25.1	253	2 S29931	RNA N-glycosidase
10	337	24.8	253	2 S28539	RNA N-glycosidase
11	336	24.8	253	2 S28542	RNA N-glycosidase
12	335.5	24.7	292	1 R10HG2	RNA N-glycosidase
13	335	24.7	293	2 S28541	RNA N-glycosidase
14	319.5	23.5	293	2 S17519	RNA N-glycosidase
15	313	23.1	316	2 J70753	RNA N-glycosidase
16	291	21.4	576	1 R1CSD	ricin D precursor
17	288.5	21.3	245	2 JCA840	RNA N-glycosidase
18	283	20.9	236	2 S17932	RNA N-glycosidase
19	271.5	20.0	564	1 R1CSAC	agglutinin precurs
20	267	18.9	278	2 A39817	RNA N-glycosidase
21	247.5	18.2	286	1 RLPUGG	RNA N-glycosidase
22	243	17.9	278	2 S23519	beta-luifin - smoo
23	241	17.8	247	2 J00393	karasurin - Mongol
24	241	17.8	289	1 R1R7T	karasurin C - ric
25	240	17.7	289	1 R1R7T	RNA N-glycosidase
26	236	17.4	247	2 JCS032	karasurin-B - ric
27	235	17.3	250	2 T2LSA	luifin-B - smooth
28	230.5	17.0	528	1 JZL018	abrin-a precursor
29	229	16.9	527	2 S32430	abrin-b precursor

30	217.5	16.0	251	2 C39761	abrin (clone 7.2)
31	215	15.8	286	2 S25560	RNA N-glycosidase
32	211	15.5	286	2 JC4235	RNA N-glycosidase
33	209.5	15.4	528	2 S32431	abrin-d precursor
34	209.5	15.4	562	2 S16022	abrin-c precursor
35	200	14.7	254	2 PD0018	mistletoe lectin I
36	199.5	14.7	277	2 S22494	RNA N-glycosidase
37	198	14.6	570	2 S62627	agglutinin I precu
38	165.5	12.2	157	2 S17934	RNA N-glycosidase
39	148	10.9	106	2 B39761	abrin (clone 3.7)
40	131	9.7	32	2 S38528	RNA N-glycosidase
41	124.5	9.2	319	2 S15695	shiga-like toxin I
42	124	9.1	315	1 XUBPH9	Shiga-like toxin C
43	124	9.1	315	2 A53887	Shiga-like toxin I
44	121.5	9.0	319	2 I60446	Shiga-like cytotox
45	121	8.9	315	1 A28626	Shigella toxin cha

#### ALIGNMENTS

RESULT 1  
JF0401  
C:Species: Phytolacca americana (Virginian pokeweed)  
C.Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 07-May-1999  
C.Accession: JF0401  
R:Kung, S.S.; Kimura, M.; Funatsu, G.  
Agric. Biol. Chem. 54, 3301-3318, 1990  
A:Title: The complete amino acid sequence of antiviral protein from the seeds of pk  
A:Reference number: JF0401; MUID:91242096; PMID:1368643  
A:Accession: JF0401  
A:Molecule type: protein  
A:Residues: 1-261 <KUN>  
A:Experimental source: seed  
C:Comment: This protein prevents the replication of a number of plant viruses, and  
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
C:Keywords: disulfide bond; glycoprotein  
F:6-254/Domain: RNA N-glycosidase homology <RNG>  
F:10,44,255/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:34-258,84-105/Disulfide bonds: #status experimental

Query Match 80.8%; Score 1096.5; DB 2; Length 261;  
Best Local Similarity 82.8%; Pred. No. 2.8e-81;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY	2	INTTFDAGNATINKYATFMSLRNQAADPKLCYGIPLDPJNSTPYLLVLIQGANIK	61
DB	1	INTTFDAGNATINKYATFMSLRNQAADPKLCYGIPLDPJNSTPYLLVLIQGANIK	60
QY	62	TTTLMRRNNLVYMGSDPFGNKKRYHIFNDITSTERTDVNTLCSSSSSVVMSIYN	121
DB	61	TTTLMRRNNLVYMGSDPFGNKKRYHIFNDITSTERTDVNTLCSSSSSVVMSIYN	119
QY	122	SLYPMKKAENVSNNOVLTGILSSDGIKISGVDPVKTAEFFLLVATIQWSEAAKF	181
DB	120	GLYPTLEKKAGVTSNENVOIGTILSSDGIKISGVDPVKTAEFFLLVATIQWSEAAKF	179
QY	182	KYIENQVKTNFRAFYDPKVIINLEKKWKISEAIIHNKNGALPKPLEIYDAKGYKWIIVL	241
DB	180	KYIENQVKTNFRAFYDPKVIINLEKKWKISEAIIHNKNGALPKPLEIYDAKGYKWIIVL	239
QY	242	RVDENRDVALLKVNGCTCOT 263	
DB	240	RVDENRDVALLKVNGCTCOT 261	

RESULT 2  
S17757  
RNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed  
N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosor  
C:Species: Phytolacca americana (Virginian pokeweed)  
C.Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Aug-1999



Db

26 VFEDLETAKTKYKGFSLRLNIVYDSKLVYEGIMLPARIKAPVYLLAEKKAKAGDI 45

QY

61 KTTTLMRLRNLLVYMGYSDFPENGKCRHIFENDITSTERTDVENTLSCSSSRVAMSIN 120

Db

86 -TTTLVASKNDDLVVAFDTQVAG-KLRAHYFPDISLATAKAIFPT-----AVQYIQIGY 137

QY

121 NSLYPTMEKKAENVNSNOVLGQIQLSSDIGISG---VDSFPTVEAFELLVAIQMSE 177

Db

138 TSNVYIEGAGAGSN-RVNFQLGFKVKEYMVLVYGNVODSDYRSEAEKFLLAIQMAE 196

QY

178 AARFKYIENOVKTNFENRAFYPPDKYINLEEKMGKISEAIIHANKGALPKPLELVAKGTR 237

Db

197 AARFKYVESALIN-----VVPDYKVPSELENMSKISEGRKAVKVIISPPIELVANSNK 252

QY

238 WIVLRVDELINRDYALLKIV 256

Db

253 WTVNOVSDIKPDGMGILSY 271

RESULT 7

RNA N-glycosidase (EC 3.2.2.22) saporin S9 - common soapwort

C:Species: Saponaria officinalis (common soapwort)

C:Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 01-Mar-2002

C:Accession: A58923

R:Submitted to, M.: Di Maro, A.; Ferranti, P.; Bolognesi, A.; Stipe, F.; Parente, P.

R:Submitted to the Protein Sequence Database, December 1998

A:Description: Saporin-S9, the most basic ribosome-inactivating protein from *Saponaria*

A:Reference number: A58923

A:Accession: A58923

A:Molecule type: protein

A:Residues: 1-253 <MAS>

A:Experimental source: seeds

C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase; toxin

Query Match 25 3%; Score 343.5; DB 2; Length 253;

Best Local 38.4%; Pred. No. 2.1e-20;

Matches 89; Conservative 42; Mismatches 88; Indels 13; Gaps 7;

QY

2 INTITPDAGNATINKATFMESLRNQAKDPKLCYGIPI-LPDTNSTPKYLLVLOGANL 60

Db

1 VTSITLDLVPTAGQYSSFDKIRNWKDPNLKYGCTDIAGVIGPESKDFLRINFQSSR- 59

QY

61 KTTTLMRLRNLLVYMGYSDFPENGKCR-RHIENDITSTERTDVENTLSCSSSRVAMSIN 119

Db

60 GTVSLGKLRDNLVYVAYLAMDMNTNVRAYYFRSEITSAEIT---ALFPEATAAHHKALE 115

QY

120 YNSLYPTMEKKAENV---NSRNOVLGQIQLSSDIGISGVDSFPYKTEAFPLVAIQMV 175

Db

116 VTEDYHSIENAAOITEDGKSRKELGLGINLSTMTQTVNKKYRV-VKNDAKRLLIQIMT 174

QY

176 SEARFKYIENOVKTNFENRAFYPPDPYINLEEKMGKISEAIIH-NAKNGALPK 226

Db

175 AEAVERFYIQLNLTAKNPKNFSENKVIINFEVWKKIISAIHGDANKGVFNK 226

RESULT 8

RNA N-glycosidase (EC 3.2.2.22) 6 precursor - common soapwort (fragment)

C:Species: Saponaria officinalis (common soapwort)

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 20-Aug-1999

C:Accession: S05205; A33231; S17689; S16330; A45499

R:Benatti, L.; Saccardo, M.B.; Dani, M.; Nitelli, G.; Sassano, M.; Lorenzetti, R.; Lat

Eur. J. Biochem. 183; 465-470, 1989

A:Title: Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-inacti

A:Reference number: S05205; MIMD:89338421; PMID:2547612

A:Accession: S05205

A:Molecule type: mRNA

A:Residues: 1-283 <BEN>

A:Cross-references: EMBL:X15655

A:Accession: A33231

A:Molecule type: protein  
A:Residues: 49-115;206-211,'T',213;234-277 <GEN2>  
R:Fordham-Skelton, A.P.; Yarwood, A.; Croy, R.R.D.  
Mol. Gen. Genet. 221, 134-138, 1990  
A:Title: Synthesis of saporin gene probes from partial protein sequence data: use of ind  
A:Reference number: S11894; MUID:90220515; PMID:2325629  
A:Accession: S17689  
A:Molecule type: protein  
A:Residues: 25-71,'D',77-88;102-122,'L',124-154 <FOR>  
R:Lappi, D.A.; Esch, F.S.; Barbieri, L.; Stlrpe, F.; Sorla, M.  
Biochem. Biophys. Res. Commun. 129, 934-942, 1985  
A:Title: Characterization of a Saponaria officinalis seed ribosome-inactivating protein:  
A:Reference number: S16330; MUID:85251709; PMID:3925952  
A:Accession: S16330  
A:Molecule type: protein  
A:Residues: 25-41,'X',43-59,'S',61 <LAP>  
R:Barthelemy, I.; Martineau, D.; Ong, M.; Matsunami, R.; Ling, N.; Benatti, L.; Cavallari  
J. Biol. Chem. 268, 6541-6548, 1993  
A:Title: The expression of saporin, a ribosome-inactivating protein from the plant Sapor  
A:Reference number: A45499; MUID:93203250; PMID:8454624  
A:Accession: A45499  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 25-277 <BAR>  
A:Cross-references: GB:S57638; MID:9298762; PIDN:AA825863.1; PID:9298763  
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase; monomer; toxin  
E:1-24/Domain: signal sequence #status predicted <SIG>  
F:30-283/Product: RNA N-glycosidase 6 #status experimental <MAT>  
F:30-273/Domain: RNA N-glycosidase homology <RNC>  
Query Match 25.2%; Score 342; DB 2; Length 283;  
Best Local Similarity 35.9%; Pred. No. 3.2e-20;  
Matches 94; Conservative 51; Mismatches 97; Indels 20; Gaps 9;  
2 INTTFDAGNATINKVATFPMESLRNQAQKPKLCYGIPI-LPDTNSTPKYLKQCANL 60  
DB 25 VTSITLVLNPTAGQYSSFDKIRNNVNDPLKYGCTGDIIVIGPPSEKELRINFQSSR- 83  
QY 61 KTTLMRLRNLLYMGSDPFGNKR-VHIFNDITSTERTDVENTLSCSSSRVAMSIN 119  
DB 84 GTVSLGLKRDNLVYVALAMDNTVNNRAYFRSEITSAELT-----ALFPEATTAANKALE 139  
QY 120 YNSLYPTMEKKAEEV-----NSRNOVQIGIQLSSDQIGISGVDSFPVKTEAFLLVAIOMV 175  
DB 140 YTEDYQSIIEKNAQTQGDQSRKEGLGIDLLSTSMKAVN-KKARVYDEARFLLIAIOMT 198  
QY 176 SEARFXYIENOVNTNFRAPYDPKVINLEEKWKGISSEAIH-NAKNGALPKLELVDAK 234  
DB 199 AEAFRFYIOLNLTAKNPNKFNSEKVIQFEVNMKKISTAIYGDAAKNGVFNKDYDFGFGK 258  
QY 235 GTKWIIVLRVDEINRDVALLKTV 256  
DB 259 -----VRQVKDL--QMGLLMTL 273  
RESULT 9  
S29931.  
RNA N-glycosidase (EC 3.2.2.22) saporin 2 (clone G-9) - common soapwort (fragment)  
N:Alternate names: ribosome-inactivating protein; saporin 2  
C:Species: Saponaria officinalis (common soapwort)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
C:Accession: S29931  
R:Sorta, M.R.  
Submitted to the EMBL Data Library, October 1992  
A:Reference number: S28539  
A:Accession: S29931  
A:Molecule type: DNA  
A:Residues: 1-253 <SOR>  
A:Cross-references: EMBL:X69135; MID:921335; PIDN:CAA48889.1; PID:921336  
A:Experimental source: clone G-9  
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase; monomer; toxin  
F:6-249/Domain: RNA N-glycosidase homology <RNC>  
Query Match 25.18%; Score 341; DB 2; Length 253;  
Best Local Similarity 35.9%; Pred. No. 3.3e-20;  
Matches 94; Conservative 51; Mismatches 97; Indels 20; Gaps 9;  
2 INTTFDAGNATINKVATFPMESLRNQAQKPKLCYGIPI-LPDTNSTPKYLKQCANL 60  
DB 1 VTSITLVLNPTAGQYSSFDKIRNNVNDPLKYGCTGDIIVIGPPSEKELRINFQSSR- 59  
QY 61 KTTLMRLRNLLYMGSDPFGNKR-VHIFNDITSTERTDVENTLSCSSSRVAMSIN 119  
DB 60 GTVSLGLKRDNLVYVALAMDNTVNNRAYFRSEITSAELT-----ALFPEATTAANKALE 115  
QY 120 YNSLYPTMEKKAEEV-----NSRNOVQIGIQLSSDQIGISGVDSFPVKTEAFLLVAIOMV 175  
DB 116 YTEDYQSIIEKNAQTQGDQSRKEGLGIDLLSTSMKAVN-KKARVYDEARFLLIAIOMT 174  
QY 176 SEARFXYIENOVNTNFRAPYDPKVINLEEKWKGISSEAIH-NAKNGALPKLELVDAK 234  
DB 175 AEAFRFYIOLNLTAKNPNKFNSEKVIQFEVNMKKISTAIYGDAAKNGVFNKDYDFGFGK 234  
QY 235 GTKWIIVLRVDEINRDVALLKTV 256  
DB 235 -----VRQVKDL--QMGLLMTL 249  
RESULT 10  
S28539  
RNA N-glycosidase (EC 3.2.2.22) (clone G-1) - common soapwort (fragment)  
N:Alternate names: ribosome-inactivating protein; saporin  
C:Species: Saponaria officinalis (common soapwort)  
C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Aug-1999  
C:Accession: S28539  
R:Sorta, M.R.  
Submitted to the EMBL Data Library, October 1992  
A:Reference number: S28539  
A:Accession: S28539  
A:Molecule type: DNA  
A:Residues: 1-253 <SOR>  
A:Cross-references: EMBL:X69131; MID:921328; PIDN:CAA48885.1; PID:921329  
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase; toxin  
F:6-249/Domain: RNA N-glycosidase homology <RNC>  
Query Match 24.8%; Score 337; DB 2; Length 253;  
Best Local Similarity 35.5%; Pred. No. 6.9e-20;  
Matches 93; Conservative 50; Mismatches 99; Indels 20; Gaps 9;  
2 INTTFDAGNATINKVATFPMESLRNQAQKPKLCYGIPI-LPDTNSTPKYLKQCANL 60  
DB 1 VTSITLVLNPTAGQYSSFDKIRNNVNDPLKYGCTGDIIVIGPPSEKELRINFQSSR- 59  
QY 61 KTTLMRLRNLLYMGSDPFGNKR-VHIFNDITSTERTDVENTLSCSSSRVAMSIN 119  
DB 60 GTVSLGLKRDNLVYVALAMDNTVNNRAYFRSEITSAELT-----ALFPEATTAANKALE 115  
QY 120 YNSLYPTMEKKAEEV-----NSRNOVQIGIQLSSDQIGISGVDSFPVKTEAFLLVAIOMV 175  
DB 116 YTEDYQSIIEKNAQTQGDQSRKEGLGIDLLSTSMKAVN-KKARVYDEARFLLIAIOMT 174  
QY 176 SEARFXYIENOVNTNFRAPYDPKVINLEEKWKGISSEAIH-NAKNGALPKLELVDAK 234  
DB 175 AEAFRFYIOLNLTAKNPNKFNSEKVIQFEVNMKKISTAIYGDAAKNGVFNKDYDFGFGK 234  
QY 235 GTKWIIVLRVDEINRDVALLKTV 256  
DB 235 -----VRQVKDL--QMGLLMTL 249  
RESULT 11  
S28542

rRNA N-glycosidase (EC 3.2.2.22) (clone G-7) - common soapwort (fragment)

N:Alternate names: ribosome-inactivating protein; saporin

C:Species: Saponaria officinalis (common soapwort)

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Aug-1999

C:Accession: S28542

R:Soria, M.R.

submitted to the EMBL Data Library, October 1992

A:Reference number: S28539

A:Accession: S28542

A:Molecule type: DNA

A:Residues: 1-253 <SOR>

A:Cross-references: EMBL:X69134; NID:g21333; PIDN:CAA4888.1; PID:g21334

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase; toxin

F:6-249/Domain: rRNA N-glycosidase homology <RNG>

#### Query Match

24.8%; Score 336; DB 2; Length 253;

Best Local Similarity 35.5%; Pred. No. 8.3e-20;

Matches 93; Conservative 51; Mismatches 98; Indels 20; Gaps 9;

QY 2 INTTFDAGNATINKATFMESLRNQAOPKLCYGIPL-LPDTNSTPKYLLVKQANL 60

Db 1 VSTITLDLVNPTAGQYSSFDVKIRNNVNDPNLKYGTDAVIGPPSKKEFLRINFQSSR- 59

QY 61 KTTTLMLRRNNLYVMGYSDPFNGNCR-YHIFNDITSTERTDVENTLSSSSSRVAMSTN 119

Db 60 GTVSLGKLRDNLVVAIYLAAMDNTNVRAYFSEITSAELT-----ALFEATTAQKALE 115

QY 120 YNSLYPTMEKKAEEV---NSRNQVGLGIQLSSDICKISGVDSFPVKTEAFLLVAI 175

Db 116 YTEDYQSIENKNAQITGGDSRKELGIDLLTSMBAVN-KKRAYKNEARFLLIAMT 174

QY 176 SEARPKYTIENQKTFNRAFYDPKVINLEEKWKISPAIH-NAKNGALPKLELVDAK 234

Db 175 AEARPRYIQLVTKNFPKPFNSKNVIOFEVWKKRISTAIYGDAAKNGVFNKDYDFGK 234

QY 235 GTKVIPLRVDEINRDVALLKYY 256

Db 235 -----VRQVKDL--QMGLLMYL 249

#### RESULT 12

##### RLOGH2

rRNA N-glycosidase (EC 3.2.2.22) Sap2 precursor - common soapwort

N:Alternate names: ribosome-inactivating protein; saporin 2; saporin S5

C:Species: Saponaria officinalis (common soapwort)

C>Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 16-Jul-1999

C:Accession: S17933; S28540; S38526; S15459

R:Fordham-Skelton, A.P.; Taylor, P.N.; Hartley, M.R.; Crox, R.R.D.

Mol. Gen. Genet. 229, 460-466, 1991

A:Title: Characterisation of saporin genes: in vitro expression and ribosome inactivation

A:Reference number: S17932; MUID:92049247; PMID:1719367

A:Accession: S17933

A:Molecule type: DNA

A:Residues: 1-292 <FOR>

A:Cross-references: EMBL:X59255; GB:S63902; NID:g2094853; PIDN:CAA11948.1; PID:g21321

R:Soria, M.R.

submitted to the EMBL Data Library, October 1992

A:Reference number: S28539

A:Accession: S28540

A:Molecule type: DNA

A:Residues: 25-283 <SOR>

A:Cross-references: EMBL:X69132; NID:g21330; PIDN:CAA4888.1; PID:g938284

R:Ferreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; Rod

Biochim. Biophys. Acta 1216, 31-42, 1993

A:Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA

A:Reference number: S38521; MUID:94032486; PMID:8218413

A:Accession: S38526

A:Molecule type: protein

A:Residues: 25-54 <FER>

C:Genetics:

A:Gene: SAP2

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase; monomer; toxin

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-292/Product: rRNA N-glycosidase Sap2 #status predicted <MAT>

F:30-273/Domain: rRNA N-glycosidase homology <RNG>

#### Query Match

24.7%; Score 335.5; DB 1; Length 292;

Best Local Similarity 34.9%; Pred. No. 1.1e-19;

Matches 98; Conservative 47; Mismatches 101; Indels 35; Gaps 11;

QY 2 INTTFDAGNATINKATFMESLRNQAOPKLCYGIPL-LPDTNSTPKYLLVKQANL 60

Db 25 VSTITLDLVNPTAGQYSSFDVKIRNNVNDPNLKYGTDAVIGPPSKKEFLRINFQSSR- 83

QY 61 KTTTLMLRRNNLYVMGYSDPFNGNCR-YHIFNDITSTERTDVENTLSSSSSRVAMSTN 119

Db 84 GTVSLGKLRDNLVVAIYLAAMDNTNVRAYFSEITSAELT-----ALFEATTAQKALE 139

QY 120 YNSLYPTMEKKAEEV---NSRNQVGLGIQLSSDICKISGVDSFPVKTEAFLLVAI 172

Db 140 YTEDYQSIENKNAQITGGDSRKELGIDLLTSMBAVN-KKRAYKNEARFLLIAMT 195

QY 173 QWSEARPKYTIENQKTFNRAFYDPKVINLEEKWKISPAIH-NAKNGALPKLELVDAK 231

Db 196 QMTAEVARERYIQLVTKNFPKPFNSKNVIOFEVWKKRISTAIYGDAAKNGVFNKDYDFG 255

QY 232 DAKGTWIVLRVDEINRDVALLKYY-----NGTCQTT 263

Db 256 FGR-----VRQVKDL--QMGLLMYLGRKSSNEANSTAYAT 289

#### RESULT 13

##### S28541

rRNA N-glycosidase (EC 3.2.2.22) (clone G-4) - common soapwort (fragment)

N:Alternate names: ribosome-inactivating protein; saporin

C:Species: Saponaria officinalis (common soapwort)

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Aug-1999

C:Accession: S28541

R:Soria, M.R.

submitted to the EMBL Data Library, October 1992

A:Reference number: S28539

A:Accession: S28541

A:Molecule type: DNA

A:Residues: 1-253 <SOR>

A:Cross-references: EMBL:X69133; NID:g21331; PIDN:CAA4888.1; PID:g21332

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase; toxin

F:6-249/Domain: rRNA N-glycosidase homology <RNG>

#### Query Match

24.7%; Score 335; DB 2; Length 253;

Best Local Similarity 35.8%; Pred. No. 1e-19;

Matches 95; Conservative 47; Mismatches 97; Indels 26; Gaps 10;

QY 2 INTTFDAGNATINKATFMESLRNQAOPKLCYGIPL-LPDTNSTPKYLLVKQANL 60

Db 1 VSTITLDLVNPTAGQYSSFDVKIRNNVNDPNLKYGTDAVIGPPSKKEFLRINFQSSR- 59

QY 61 KTTTLMLRRNNLYVMGYSDPFNGNCR-YHIFNDITSTERTDVENTLSSSSSRVAMSTN 119

Db 60 GTVSLGKLRDNLVVAIYLAAMDNTNVRAYFSEITSAELT-----ALFEATTAQKALE 115

QY 120 YNSLYPTMEKKAEEV---NSRNQVGLGIQLSSDICKISGVDSFPVKTEAFLLVAI 172

Db 116 YTEDYQSIENKNAQITGGDSRKELGIDLLTSMBAVN-KKRAYKNEARFLLIAMT 171

QY 173 QWSEARPKYTIENQKTFNRAFYDPKVINLEEKWKISPAIH-NAKNGALPKLELVDAK 231

Db 172 QMTAEVARERYIQLVTKNFPKPFNSKNVIOFEVWKKRISTAIYGDAAKNGVFNKDYDFG 231

QY 232 DAKGTWIVLRVDEINRDVALLKYY 256

Db 232 FGR-----VRQVKDL--QMGLLMYL 249



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 19.8805 Seconds

(without alignments)  
730.581 Million cell updates/sec

Title: US-09-978-274A-4\_COPY\_155\_263

Perfect score: 564  
Sequence: 1 GVDSFPVKTEAFFLLVAIQ.....DEINRDVALLKYNGTCQT 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

```
Minimum DB seq length: 0
```

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Maximum Match 100%  
Listing first 45 summaries

```
Database :
A_Genecore_101002 : *
1 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT : *
2 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT : *
3 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT : *
4 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT : *
5 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT : *
6 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT : *
7 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT : *
8 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT : *
9 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT : *
10 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT : *
11 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT : *
12 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT : *
13 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT : *
14 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT : *
15 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT : *
16 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT : *
17 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT : *
18 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT : *
19 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT : *
20 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT : *
21 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT : *
22 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT : *
23 : /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT : *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	457	81.0	294	14	AAR37425	Pokeweed antiviral
2	454	80.5	224	18	AAW14255	Mature pokeweed an
3	454	80.5	225	18	AAW14254	Mature pokeweed an
4	454	80.5	226	18	AAW14253	Mature pokeweed an
5	454	80.5	227	18	AAW14252	Mature pokeweed an
6	454	80.5	228	18	AAW14251	Mature pokeweed an
7	454	80.5	229	18	AAW14250	Mature pokeweed an
8	454	80.5	230	18	AAW14249	Mature pokeweed an
9	454	80.5	231	18	AAW14248	Mature pokeweed an
10	454	80.5	232	18	AAW14247	Mature pokeweed an

11	454	80.5	233	18	AAW14246	Mature pokeweed an
12	454	80.5	234	18	AAW14245	Mature pokeweed an
13	454	80.5	235	18	AAW14244	Mature pokeweed an
14	454	80.5	236	18	AAW14243	Mature pokeweed an
15	454	80.5	237	18	AAW14242	Mature pokeweed an
16	454	80.5	238	18	AAW14241	Mature pokeweed an
17	454	80.5	239	18	AAW14240	Mature pokeweed an
18	454	80.5	240	18	AAW14239	Mature pokeweed an
19	454	80.5	241	18	AAW14238	Mature pokeweed an
20	454	80.5	242	18	AAW14237	Mature pokeweed an
21	454	80.5	243	18	AAW14236	Mature pokeweed an
22	454	80.5	244	18	AAW14235	Mature pokeweed an
23	454	80.5	245	18	AAW14234	Mature pokeweed an
24	454	80.5	246	18	AAW14233	Mature pokeweed an
25	454	80.5	247	18	AAW14232	Mature pokeweed an
26	454	80.5	248	18	AAW14231	Mature pokeweed an
27	454	80.5	249	18	AAW14230	Mature pokeweed an
28	454	80.5	250	18	AAW14229	Mature pokeweed an
29	454	80.5	251	18	AAW14228	Mature pokeweed an
30	454	80.5	252	18	AAW14227	Mature pokeweed an
31	454	80.5	253	18	AAW14226	Mature pokeweed an
32	454	80.5	254	18	AAW14225	Mature pokeweed an
33	454	80.5	255	18	AAW14224	Mature pokeweed an
34	454	80.5	256	18	AAW14223	Mature pokeweed an
35	454	80.5	257	18	AAW14222	Mature pokeweed an
36	454	80.5	258	18	AAW14221	Mature pokeweed an
37	454	80.5	259	18	AAW14220	Mature pokeweed an
38	454	80.5	260	18	AAW14219	Mature pokeweed an
39	454	80.5	261	18	AAW14218	Mature pokeweed an
40	454	80.5	262	18	AAW14164	Mature pokeweed an
41	454	80.5	262	18	AAW14163	Mature pokeweed an
42	454	80.5	262	15	AAW57152	Wild-type Pokeweed
43	454	80.5	292	15	AAW57153	Pokeweed Antiviral
44	454	80.5	313	15	AAW48548	Sequence of Phytol
45	454	80.5	313	21	AAW58025	Wild-type pokeweed

ALIGNMENTS

RESULT 1

AAW37345

AAW37345 standard; Protein: 294 AA.

XX ID AAW37345:

XX AC

XX DT 09-NOV-1993 (first entry)

XX DE Pokeweed antiviral protein.

XX KW Pokeroot; ricin; protein synthesis inhibitor; cancer; polymerase chain reaction; PCR.

XX OS Phytolacca americana.

XX FH Key

XX FT Peptide

XX FT Protein

XX FT

XX FT

XX FT

XX PN JP05137580-A.

XX PD 01-JUN-1993.

XX PE 20-NOV-1991; 91JP-0329672.

XX PR 20-NOV-1991; 91JP-0329672.

XX PA (NISB ) JAPAN TOBACCO INC.

XX WP1: 1993-211306/26.

XX N-PSDB: AAQ43967.

```

XX  New pokeweed antiviral protein (PAP) with similar activity to
PT  ricin - used to treat cancer and as an agricultural chemical
XX
XX  Claim 1; Page 11-13; 14pp; Japanese.
XX
CC  NB: A protein comprising 261 amino acids is claimed.
CC  PAP has a similar activity to ricin, i.e. inhibits protein synthesis.
CC  The protein may be obtained all year round by recombinant DNA
CC  techniques. PAP can be used partic. against cancer and as an
CC  agricultural chemical.
CC  Total mRNA, is extracted from the seeds, leaves and roots of
CC  pokeweed and used to prepare cDNA using PCR. The resultant cDNA is
CC  used to prepare two DNA fractions, which are introduced into a
CC  cloning vector EMBL3 and then into host E.coli PLK-17 (p2) to
CC  produce PAP.
CC
XX  Sequence 294 AA:
SQ
XX
XX  Query Match 81.0%; Score 457; DB 14; Length 294;
XX  Best Local Similarity 82.6%; Pred. No. 7,8e-47;
XX  Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0
XX
QY 1 GVDSFVKEAPFLVLAIGMSEARFKYIENOVKTNRRAFYPPKINIEEKWKISE 60
Db 177 GVDSFTEKTEAEFLVLAIGMSEARFKYIENOVKTNRRAFYPPKAXLNLEESWGKIST 236
QY 61 AIHNANNGALPKPELVDAKGTKMWIVLRVDEINRQVALTKVNGTCOTT 109
Db 237 AIHNANNGALTSPLELKNMNGSKWIVLRVDIPEVGLTKVNGTCOAT 285
XX
XX  RESULT 2
XX  AAM14255
XX  ID AAM14255 standard; protein; 224 AA.
XX
XX  AAM14255:
XX
XX  25-JUN-1997 (first entry)
XX
XX  Mature pokeweed antiviral protein deletion variant (39-262).
XX
XX  Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
KW  anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KW  stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KW  translation; broad spectrum; resistance; cell death; sterility; nematode;
KM  bacterium.
XX
XX  Phytolacca americana.
XX
XX  MO9703183-A1.
XX
XX  30-JAN-1997.
XX
XX  11-JUL-1996; 96MO-US11546.
XX
XX  11-JUL-1995; 95US-0500694.
XX  11-JUL-1995; 95US-0500611.
XX
XX  (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX  Turner NE;
XX  PI
XX  WPI: 1997-119040/11.
XX
XX  New pokeweed antiviral protein mutants - which exhibit anti-viral
PT  and anti-fungal activity in plants and have reduced phytotoxicity
XX
XX  Claim 14; -: 64pp; English.
XX
XX  Proteins AAM14163-1414256 represent new pokeweed antiviral protein (PAP)
CC  mutants having reduced phytotoxicity but retaining anti-viral or
CC  anti-fungal activity in plants. The sequences' numbering corresponds to

```

[illegible]



CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

XX Sequence 225 AA:

Query Match 80.5%; Score 454; DB 18; Length 225;  
 Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSPVKTAEFFLLVAIQWSEARFKYIENOVKTNFRAPYPPKVINLEKKKISF 60  
 DB 117 GVMSTFKTEAEFFLLVAIQWSEARFKYIENOVKTNFRAPYPPKVINLEKKKIST 176  
 OY 61 AIHNAKNGALPKPLELVDAKGTKWIVLRVDEINRVALLKYNGTCQTT 109  
 DB 177 AIHDAKNGVLPKPLELVDAKGTKWIVLRVDEINRVALLKYNGSCQTT 225

#### RESULT 4

AAM14253  
 ID AAM14253 standard; protein: 226 AA.

XX AAM14253;

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (37-262).

KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KM bacterium.

OS Phytolacca americana.

PN WO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Tumor NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14: -; 64pp; English.

XX Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal

CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

XX Sequence 226 AA:

Query Match 80.5%; Score 454; DB 18; Length 226;  
 Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSPVKTAEFFLLVAIQWSEARFKYIENOVKTNFRAPYPPKVINLEKKKISF 60  
 DB 118 GVMSTFKTEAEFFLLVAIQWSEARFKYIENOVKTNFRAPYPPKVINLEKKKIST 177  
 OY 61 AIHNAKNGALPKPLELVDAKGTKWIVLRVDEINRVALLKYNGTCQTT 109  
 DB 178 AIHDAKNGVLPKPLELVDAKGTKWIVLRVDEINRVALLKYNGSCQTT 226

#### RESULT 5

AAM14252  
 ID AAM14252 standard; protein: 227 AA.

XX AAM14252;

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (36-262).

KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KM bacterium.

OS Phytolacca americana.

PN WO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Tumor NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14: -; 64pp; English.

XX Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a

line 285 tRNA of eukaryotic ribosomes and also interferes with elongation

lactoferrin broad

**Claim 14:** -; 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP) mutants having reduced phytotoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-W14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. prior to processing, the protein contains a 22 amino acid N-terminal signal sequence and a 29 amino acid C-terminal extension. PAP is a type I ribosomal inhibitor protein (RIP) that catalyses the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can confer broad spectrum virus and fungus resistance to plants without

CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SQ Sequence 229 AA:  
Query Match 80.5%; Score 454; DB 18; Length 229;  
Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
OY 1 GVDSPVKTAEFFLLVAIOMVSEARFKYIENQVKTNNRFPDPKVINLEKKGKISE 60  
DB 121 GVSFTEKTEAEFFLLVAIOMVSEARFKYIENQVKTNNRFPDPKVINLEOTWKGKIST 180  
OY 61 AHNNAKNGALPKPLELDVDAKGKMTVLRVDEINRVDALLKYNGTCOTT 109  
DB 181 AHDKAKNGVLPKPLELDVDAKSAKMTVLRVDEIKPVDALLNYGSGCOTT 229  
RESULT 8  
AAW14249  
ID AAW14249 standard; protein: 230 AA.  
XX  
AC AAW14249:  
XX  
DT 25-JUN-1997 (first entry)  
XX  
DE Mature pokeweed antiviral protein deletion variant (33-262).  
XX  
KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
XX  
OS Phytolacca americana.  
XX  
PN WO9703183-A1.  
XX  
PD 30-JAN-1997.  
XX  
PF 11-JUL-1996; 96WO-US11546.  
XX  
PR 11-JUL-1995; 95US-0500694.  
XX  
PR 11-JUL-1995; 95US-0500611.  
XX  
PA (RUF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Turner NE;  
XX  
DR WPI: 1997-119040/11.  
XX  
PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity.  
XX  
PS Claim 14: -; 64pp; English.  
XX  
CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.

CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SQ Sequence 230 AA:  
Query Match 80.5%; Score 454; DB 18; Length 230;  
Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
OY 1 GVDSPVKTAEFFLLVAIOMVSEARFKYIENQVKTNNRFPDPKVINLEKKGKISE 60  
DB 122 GVSFTEKTEAEFFLLVAIOMVSEARFKYIENQVKTNNRFPDPKVINLEOTWKGKIST 181  
OY 61 AHNNAKNGALPKPLELDVDAKGKMTVLRVDEINRVDALLKYNGTCOTT 109  
DB 182 AHDKAKNGVLPKPLELDVDAKSAKMTVLRVDEIKPVDALLNYGSGCOTT 230  
RESULT 9  
AAW14248  
ID AAW14248 standard; protein: 231 AA.  
XX  
AC AAW14248:  
XX  
DT 25-JUN-1997 (first entry)  
XX  
DE Mature pokeweed antiviral protein deletion variant (32-262).  
XX  
KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
XX  
OS Phytolacca americana.  
XX  
PN WO9703183-A1.  
XX  
PD 30-JAN-1997.  
XX  
PF 11-JUL-1996; 96WO-US11546.  
XX  
PR 11-JUL-1995; 95US-0500694.  
XX  
PR 11-JUL-1995; 95US-0500611.  
XX  
PA (RUF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Turner NE;  
XX  
DR WPI: 1997-119040/11.  
XX  
PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
PS Claim 14: -; 64pp; English.  
XX  
CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.

XX Sequence 231 AA:  
SQ Query Match 80.5%; Score 454; DB 18; Length 231;  
Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSPVKTEAEFFLLVAIQMVSEARFKYIENQVKTNFNRAFPDPKVINLEEKWKISE 60  
DB 123 GWSFTEKTEAEFFLLVAIQMVSEARFKYIENQVKTNFNRAFPDPKVINLEEKWKISE 182  
OY 61 AIHNKNGALPKPPELVDAKGTWKIVLRVDEINRDVALLKYNGTCQTT 109  
DB 183 AIHDAKNGLVLPKPELVDAKGTWKIVLRVDEIKPDVALLNYGGSCOTT 231

RESULT 10  
AAW14247  
ID AAW14247 standard; protein: 232 AA.  
XX AAW14247;  
XX  
XX  
DT 25-JUN-1997 (first entry)  
XX  
XX Mature pokeweed antiviral protein deletion variant (31-262).  
DE  
XX Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;  
KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
KM bacterium.  
XX  
XX  
OS Phytolacca americana.  
XX  
XX  
PN MO9703183-A1.  
XX  
XX 30-JAN-1997.  
PD  
XX  
XX 11-JUL-1996; 96WO-US11546.  
PF  
XX  
XX 11-JUL-1995; 95US-0500694.  
PR  
XX 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PA  
XX  
XX  
PI Tumor NE;  
XX  
XX  
DR WPI: 1997-119040/11.  
XX  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
XX  
XX  
PS Claim 14: -; 64pp; English.  
XX  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
XX  
SQ Sequence 232 AA;

XX Sequence 233 AA:  
SQ Query Match 80.5%; Score 454; DB 18; Length 233;  
Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSPVKTEAEFFLLVAIQMVSEARFKYIENQVKTNFNRAFPDPKVINLEEKWKISE 60  
DB 124 GWSFTEKTEAEFFLLVAIQMVSEARFKYIENQVKTNFNRAFPDPKVINLEEKWKISE 183  
OY 61 AIHNKNGALPKPPELVDAKGTWKIVLRVDEINRDVALLKYNGTCQTT 109  
DB 184 AIHDAKNGLVLPKPELVDAKGTWKIVLRVDEIKPDVALLNYGGSCOTT 232

RESULT 11  
AAW14246  
ID AAW14246 standard; protein: 233 AA.  
XX AAW14246;  
XX  
XX  
XX  
DT 25-JUN-1997 (first entry)  
XX  
XX Mature pokeweed antiviral protein deletion variant (30-262).  
DE  
XX Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;  
KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
KM bacterium.  
XX  
XX  
OS Phytolacca americana.  
XX  
XX  
PN MO9703183-A1.  
XX  
XX 30-JAN-1997.  
PD  
XX  
XX 11-JUL-1996; 96WO-US11546.  
PF  
XX  
XX 11-JUL-1995; 95US-0500694.  
PR  
XX 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PA  
XX  
XX  
PI Tumor NE;  
XX  
XX  
DR WPI: 1997-119040/11.  
XX  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
XX  
XX  
PS Claim 14: -; 64pp; English.  
XX  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
XX  
SQ Sequence 233 AA;

```

Best Local Similarity 82.6%; Pred. No. 1,3e-46; Indels 0; Gaps 0;
Matches 90; Conservative 5; Mismatches 14;
QY      1 GVDSFPVKTAEFFLLAIQWNSSEARFKYIENOVKTNFNRAFYDPDKVINLEEKMGKISE 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      125 GVMSEFTEKTEAEFLVAIQWNSSEARFKYIENOVKTNFNRAFNPNPKVLNLOETMKGIST 184
OY      61 AIHNAKKGALPKPLELVDAKCTKNIVLRVDINDVALLKVKVNTCQT 109
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      185 AIHDAAKKGVLPKPPLSLVDASAGAKWIVLRVDEIKPDVALLNLYVGSCQT 233

RESULT 12
AAWI4245
ID      AAWI4245 standard; protein; 234 AA.
AC      AAWI4245;
XX      AAWI4245;
DT      25-JUN-1997 (first entry)
XX      Mature pokeweed antiviral protein deletion variant (29-262).
DE      Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
XX      anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KW      stem-loop; 26S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KM      translation; broad spectrum; resistance; cell death; sterility; nematode;
KV      bacterium.
XX      Phytolacca americana.
OS      Wo9703183-A1.
XX      PN
XX      30-JAN-1997.
XX      PD
XX      PF 11-JUL-1996; 96WO-US11546.
XX      PR 11-JUL-1995; 95US-0500694.
XX      PR 11-JUL-1995; 95US-0500611.
XX      PA
XX      (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
PI      Turner NE;
DR      WPI; 1997-119040/11.
XX      PT New pokeweed antiviral protein mutants - which exhibit anti-viral
XX      and anti-fungal activity in plants and have reduced phytotoxicity
XX      Claim 14; -: 64pp; English.
XX      PS Proteins AAWI4163-WI4256 represent new pokeweed antiviral protein (PAP)
XX      mutants having reduced phytotoxicity but retaining anti-viral or
XX      anti-fungal activity in plants. The sequences' numbering corresponds to
XX      the 262 amino acid mature protein. The proteins AAWI4165-WI4217
XX      represent serial deletions from the C-terminus whereas sequences
XX      AAWI4218-55 are serial deletions from the N-terminus. Prior to
XX      processing, the protein contains a 22 amino acid N-terminal signal
XX      sequence and a 29 amino acid C-terminal extension. PAP is a type I
XX      ribosomal inhibitor protein (RIP) that catalyses the removal of a
XX      specific adenosine residue from a highly conserved stem-loop structure in
XX      the 28S rRNA of eukaryotic ribosomes and also interferes with elongation
XX      factor-2 binding thus blocking protein translation. The PAP mutants can
XX      confer broad spectrum virus and fungus resistance to plants without
XX      causing plant cell death or sterility. They can also confer increased
XX      resistance to insects, bacteria and nematodes in plants.
CC      N.B. This sequence is not given in the specification but is generated
CC      from the wild type sequence reproduced in the specification.
SQ      Sequence 234 AA;
Query Match 80.5%; Score 454; DB 18; Length 234;
Best Local Similarity 82.6%; Pred. No. 1.3e-46; Indels 0; Gaps 0;
Matches 90; Conservative 5; Mismatches 14;

```

Oy		J	GVSDFPVKTEAFELVIAIQWVSEARPKYIENOVKTNFNRAFYDDPVIINLEEKWKISE	60
Dd		126	GWSFETKEAEFLVIAIQWVSEARPKYIENOVKTNFNRAFPNPVYLQETWGKIST	185
Oy		61	AIHAKNGALPKPLELVDAGKCFKWIVLYRDEINEDVALIKVYNCTCOTT	109
Dd		186	AIHAKNGVLPRKPLELVDASGAKMIVLYRVEIKRPDALLNVVGSCQTT	234
 RESULT 13 AAW14244 ID AAW14244 standard; protein: 235 AA.				
XX	AC	AAW14244:		
XX	DT	25-JUN-1997	(first entry)	
XX	DE	Mature pokeweed antiviral protein deletion variant (28-262).		
KW	KM	Pokeweed antiviral protein: mutant; phytotoxicity; anti-viral; virus;		
XX	KM	anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;		
KW	KM	stem-loop; 2S rRNA; eukaryotic; ribosome; elongation factor-2 binding;		
KM	KM	translation; broad spectrum; resistance; cell death; sterility; nematode;		
XX	XX	bacterium.		
OS	CS	Phytolacca americana.		
XX	PN	MO9703183-A1.		
PD	PN	30-JAN-1997.		
XX	PF	11-JUL-1996;	96WC-US11546.	
PR	PR	11-JUL-1995;	95US-0500694.	
XX	XX	11-JUL-1995;	95US-0500611.	
PA	PA	(RUTF ) UNIV RUTGERS STATE NEW JERSEY.		
PI	PI	Turner NE;		
DK	DK	WPI; 1997-119040/11.		
PT	PT	New pokeweed antiviral protein mutants - which exhibit anti-viral		
XX	XX	and anti-fungal activity in plants and have reduced phytotoxicity		
PS	PS	Claim 14; -: 64pp: English.		
XX	XX	Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)		
CC	CC	mutants having reduced phytotoxicity but retaining anti-viral or		
CC	CC	anti-fungal activity in plants. The sequences' numbering corresponds to		
CC	CC	the 262 amino acid mature protein. The proteins AAW14165-W14217		
CC	CC	represent serial deletions from the C-terminus whereas sequences		
CC	CC	AAW14218-55 are serial deletions from the N-terminus. Prior to		
CC	CC	sequencing, the protein contains a 22 amino acid N-terminal signal		
CC	CC	sequence and a 29 amino acid C-terminal extension. PAP is a type I		
CC	CC	ribosomal inhibitor protein (RIP) that catalyses the removal of a		
CC	CC	specific adenosine residue from a highly conserved stem-loop structure in		
CC	CC	the 28S rRNA of eukaryotic ribosomes and also interferes with elongation		
CC	CC	factor-2 binding thus blocking protein translation. The PAP mutants can		
CC	CC	confer broad spectrum virus and fungus resistance to plants without		
CC	CC	causing plant cell death or sterility. They can also confer increased		
CC	CC	resistance to insects, bacteria and nematodes in plants.		
CC	CC	N.B. This sequence is not given in the specification but is generated		
CC	CC	from the wild type sequence reproduced in the specification.		
SO	SO	Sequence 235 AA:		
Query Match		80.5%; Score 454; DB 18; Length 235;		
Best Local Similarity		82.6%; Pred. No. 1.3e-46;		
Matches	90; Conservative	5; Mismatches 14; Indels 0; Gaps 0;		
Oy		1 GVSDFPVKTEAFELVIAIQWVSEARPKYIENOVKTNFNRAFYDDPVIINLEEKWKISE	60	



Wed Jul 2 12:18:57 2003

us-09-978-274a-4\_copy\_155\_263.rag

Page 9

```

Db      189  A|H|D|A|K|N|G|V|L|P|K|P|L|E|V|D|A|S|G|A|K|W|I|V|L|R|Y|D|E|I|K|P|D|V|A|L|N|Y|V|G|S|C|O|T|T| 237

```

Search completed: July 2, 2003, 11:39:41  
Job time : 20.8805 secs

[illegible]

ID	AA857154	standard; protein
XX	AA857154:	
AC	22-FEB-1995	(first entry)
XX	AA857154:	
DT	Pokeweed Antiviral Protein mutant PAP-9.	
XX	Pokeweed antiviral protein; PAP; ribosome inactivating protein.	
DE	Pokeweed antitumor toxin; cell targeting; mutant.	
XX	RIP type I; immunotoxin;	
KM	phytolacca americana.	
XX	location/Qualifiers	
OS	196	"wild-type Phe is replaced by Arg"
XX	key-difference	/note=
EH	Misc-difference	211 "wild-type Lys is replaced by Arg"
FT	Misc-difference	/note=
FT	Misc-difference	/note=
FT	Misc-difference	/note=
XX	FR2699553-A.	
PN	24-JUN-1994.	
XX	92F8-0014821.	
PD	24-JUN-1994.	
XX	92F8-0014821.	
PF	09-DEC-1992:	
XX	92F8-0014821.	
XX	09-DEC-1992:	
PR	WJdence J;	
XX	(INNO-) INNOTHERAPIE LAB.	
PA	Gres E,	
XX	Dore J,	
PI	1994-22165/28.	
XX	WPI: 1994-22165/28.	
DR	Gene encoding mutant protein toxic to eukaryotic	
XX	prokaryotic cells esp. mutant pokeweed anti-	
PT	useful in immunotoxin prodn.,	
PT	protection ad'	



PT and for targeted cell destruction  
 XX Claim 10, Fig 1, 25pp: French.  
 PS  
 CC Mutants of type I Ribosome Inactivating Proteins which are toxic to  
 CC eukaryotic, but not prokaryotic, cells.  
 CC the wild-type Pokeweed antiviral protein (PAP) is preferably derived from  
 CC Arg replacing wild-type Lys at positions 196 and 211, respectively.  
 CC Sequence 292 AA:  
 Query Match  
 Best Local Similarity 75.8%; Score 601; DB 15; Length 292;  
 Matches 111; Conservative 23; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MINTTFDAGNATINKYATFMEISLRNOKDKLCYGIPLMPTNSTPKYLLVLOQANL 60  
 Db 1 VNTIIIVGSTTISKYATFPLNDLRNEADPSLKCIGIPLMPTNTNPKYLLVLELOG 60  
 QY 61 KTTTLMRRNNLYVWGYSDFPFGNCKRYHIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 Db 61 KTTTLMRRNNLYVWGYSDFPFGNCKRYHIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 QY 121 NSLYPTMEKKAENVSRNOVOLGIGIILSSDICKIS 154  
 Db 121 NSLYPTMEKKAENVSRNOVOLGIGIILSSDICKIS 154  
 RESULT 10  
 AAM14217 standard; protein: 184 AA.  
 AAM14217  
 ID AAM14217  
 AC AAM14217  
 XX 25-JUN-1997 (first entry)  
 DE Mature pokeweed antiviral protein deletion variant (1-184).  
 XX Pokeweed antiviral protein deletion variant (1-184).  
 KW anti-fungal; fungus; mutant: phytoxicity; anti-viral; virus;  
 KW stem-loop; 28S rRNA; plant; ribosomal inhibitor protein; adenine; insect;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 XX bacterium.  
 OS Phytotheca americana.  
 PN M09703183-A1.  
 PD 30-JAN-1997.  
 XX 11-JUL-1996; 96MO-US11546.  
 PR 11-JUL-1995; 95US-0500694.  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 XX Turner NE;  
 PI WPI: 1997-119040/11.  
 DR New pokeweed antiviral protein mutants - which exhibit anti-viral  
 XX and anti-fungal activity in plants and have reduced phytotoxicity  
 PT Claim 8; -; 64pp: English.  
 PS Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC anti-fungal activity reduced phytotoxicity but retaining anti-viral or  
 CC the 262 amino acid mature protein. The sequences numbering corresponds to  
 CC represent serial deletions from the C-terminus whereas sequences

us-09-978-274a-6.rag  
 CC AAM14218-55 are serial deletions from the N-terminus.  
 CC processing, the protein contains a 22 amino acid N-term.  
 CC sequence and a 29 amino acid C-terminal extension.  
 CC the 28S rRNA of eukaryotic cells that catalyzes the  
 CC factor-2 binding thus blocking ribosomes and also interferes  
 CC causing broad spectrum virus and fungus resistance. The  
 CC resistance to insects, bacteria and nematodes in plants  
 CC from the wild type sequence reproduced in the specification.  
 CC Sequence 184 AA:  
 Query Match  
 Best Local Similarity 71.9%; Score 596; DB 18; Length 184;  
 Matches 110; Conservative 23; Mismatches 20; Indels 0;  
 QY 2 INTTFDAGNATINKYATFMEISLRNOKDKLCYGIPLMPTNSTPKYLLVLOQANL 60  
 Db 2 INTTFDAGNATINKYATFMEISLRNOKDKLCYGIPLMPTNSTPKYLLVLOQANL 60  
 QY 1 VNTIIIVGSTTISKYATFPLNDLRNEADPSLKCIGIPLMPTNTNPKYLLVLELOG 60  
 Db 1 VNTIIIVGSTTISKYATFPLNDLRNEADPSLKCIGIPLMPTNTNPKYLLVLELOG 60  
 QY 62 TTTTLMRRNNLYVWGYSDFPFGNCKRYHIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 Db 62 TTTTLMRRNNLYVWGYSDFPFGNCKRYHIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 QY 61 KTTTLMRRNNLYVWGYSDFPFGNCKRYHIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 Db 61 KTTTLMRRNNLYVWGYSDFPFGNCKRYHIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 QY 122 SLYPTMEKKAENVSRNOVOLGIGIILSSDICKIS 154  
 Db 122 SLYPTMEKKAENVSRNOVOLGIGIILSSDICKIS 154  
 RESULT 11  
 AAM14216 standard; protein: 185 AA.  
 AAM14216  
 ID AAM14216  
 AC AAM14216  
 XX 25-JUN-1997 (first entry)  
 DE Mature pokeweed antiviral protein deletion variant (1-185).  
 XX Pokeweed antiviral protein deletion variant (1-185).  
 KW anti-fungal; fungus; mutant: phytoxicity; anti-viral; virus;  
 KW stem-loop; 28S rRNA; plant; ribosomal inhibitor protein; adenine; insect;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 XX bacterium.  
 OS Phytotheca americana.  
 PN M09703183-A1.  
 PD 30-JAN-1997.  
 XX 11-JUL-1996; 96MO-US11546.  
 PR 11-JUL-1995; 95US-0500694.  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 XX Turner NE;  
 PI WPI: 1997-119040/11.  
 DR New pokeweed antiviral protein mutants - which exhibit anti-viral  
 XX and anti-fungal activity in plants and have reduced phytotoxicity  
 PT Claim 8; -; 64pp: English.  
 PS Proteins AAM14163-W14256 represent  
 CC anti-fungal activity reduced phytotoxicity

DB 239 TTINPALOLISPSNDPMVWVKVSIQISPMGILKF 272

## RESULT 15

ID 093Y65 PRELIMINARY: PRT: 294 AA.

AC 093Y65; 01-DEC-2001 (TRENBLREL. 19, Created)

DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)

DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)

DE rRNA - glycosidase (EC 3.2.2.22).

OS Dianthus chinensis.

OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.

OX NCBI\_TaxID=118431;

RN [1]

RP SEQUENCE FROM N.A. MEDLINE-20306826; PubMed-10850653;

RA Cho H.J., Lee S.J., Kim S., Kim B.D.;

RT "Isolation and characterization of cDNAs encoding ribosome

RT inactivating protein from *Dianthus sinensis* L.";

RL Mol. Cells 10:135-141(2000).

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.

DR EMBL: AF219237; AAK68928.1; "

DR InterPro: IPR001574; RIP.

DR Pfam: PF00161; RIP; 1.

KW Hydrolase; Toxin.

SQ SEQUENCE 294 AA: 3331 MW; 659E72DD647A72D0 CRC64:

Query Match 30.2% Score 170.5; DB 10; Length 294;

Best Local Similarity 55.2% Pred. No. 3.9e-10;

Matches 37; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

OY 7 VKTEAFFLLVAIQVSEARPKYIENQYTNFNRAFYPPKVINLEEKWKISEAIIH-NA 65

DB 185 VKDEARFLLIGIQMSAEAVRFRIQNLVTRNFPKKFNSDNTVIOYQTSWGKISEAIIHSDC 244

OY 66 KNGALPK 72

DB 245 KNGKFNK 251

Search completed: July 2, 2003, 11:42:09

Job time : 16.7673 secs

```

Query Match          36.8% Score 207.5: DB 10; Length 279;
Best Local Similarity 47.4% Pred No. 3.9e-14;
Matches 46; Conservative 15; Mismatches 29; Indels 7; Gaps 2

OY      8 KTEAFFLLVAIOMSEARFRFYIENQ--VKTNFNRAFPDPDKVILLEKMGKISEAIIHNA 65
       ||| ||| ||| ||| ||| ||| ||| ||| : | | | | | | | | | | | | | | | |
Db      187 QTEARFLLIAIQWAEARFRFYIGRAIVTTAPN-----DHIILSLENNMGALSGIRNA 241
              : | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      66 KNGALPKPLELVDAKGTWKIVLRVDEINRDVALLKYY 102
              : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      242 VKKVINPEITLQYPDGKFWITVOVSVDXKNDGMLKKYY 278
              : | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
ID      ID      PRELIMINARY: PRT: 279 AA.
09AUUE3 09AUUE3 AC
09AUUE3:
DT      01-JUN-2001 (Tremblrel. 17, Created)
DT      01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT      01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE      rRNA_glycosidase (EC 3.2.2.22).
OS      CAP30B.
OC      Chenopodium album (Lamb's-quarters).
CC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
OC      Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium.
OX      NCBI_TaxID=3559;
RN      [1]
RM      SEQUENCE FROM N.A.
RP      Park J.S., Lee S.M., Kim Y.T., Cho K.J.;
RT      "Molecular characterization of a new cDNA clone encoding a ribosome-
RL      inactivating protein (CAP30B) from Chenopodium album.";
RT      Submitted (Feb-2000) to the EMBL/Genbank/DDJ databases.
CC      -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC      SPECIFIC ADENOSINE ON THE 28S RNA.
CC      -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR      EMBL: AF230812; AAK28323.1; -.
DR      HSSP: O03464; IAPA.
DR      InterPro: IPR001574; RIP.
DR      Pfam: PF00161; RIP_1.
DR      PRINTS: PRO0396; SHIGARICIN.
KW      Hydrolase; Toxin..
SQ      SEQUENCE 279 AA; 31419 MW; 97E934F22C8033AF CRC64;

Query Match          35.0% Score 197.5: DB 10; Length 279;
Best Local Similarity 45.4% Pred No. 4.6e-13;
Matches 44; Conservative 17; Mismatches 29; Indels 7; Gaps 2

OY      8 KTEAFFLLVAIOMSEARFRFYIENQ--VKTNFNRAFPDPDKVILLEKMGKISEAIIHNA 65
       ||| ||| ||| ||| ||| ||| ||| ||| : | | | | | | | | | | | | | | | |
Db      187 QTEARFLLIAIQWAEARFRFYIGRAIVTTAPN-----NKIYSLLENMGALSGIRNA 241
              : | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      66 KNGALPKPLELVDAKGTWKIVLRVDEINRDVALLKYY 102
              : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      242 VKKVINPEITLQYPDGKFWITVOVSVDXKNDGMLKKYY 278
              : | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
ID      ID      PRELIMINARY: PRT: 541 AA.
041174 041174 AC
041174:
DT      01-NOV-1996 (Tremblrel. 01, Created)
DT      01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT      01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE      rRNA_glycosidase (EC 3.2.2.22) (Fragment).
OS      Ricinus communis (Castor bean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids I; Malpighiales; Euphorbiales; Euphorbiaceae; Ricinus.
OX      NCBI_TaxID=3988;
RN      [1]
RM      SEQUENCE FROM N.A.

```

```

RX MEDLINE-92338377; PubMed-1633311.
RA Roberts L.M., Tregear J.W., Lord J.M.;
RT "Molecular cloning of Ricin."
RT Targeted Diagn. Ther. 7:81-97(1992).
CC -I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL; S40366; AAB22582.1; -.
DR HSSP; P02879; IBR6.
DR InterPro; IPRO00772; Ricin_E-lectin.
DR InterPro; IPRO01574; RIP.
DR InterPro; IPRO01400; Somatotropin.
DR Pfam; PF00652; Ricin_B-lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SMO0458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
KW Hydrolyase; toxin.
FT NON_TER
SQ SEQUENCE 541 AA; 60281 MW; 287B2CDEF1F2E9D CRC64;

Query Match 34.0%; Score 192; DB 10; Length 541;
Best Local Similarity 39.8%; Pred. No. 4,1e-12;
Matches 41; Conservative 19; Mismatches 39; Indels 4; Gaps 2.

QY 1 GVDSFPVTEAFFLLVAIQWSEARFYKFIENQVT--NFNRAFDPDKVINLEEKMGKI 58
DB 157 GGTLQPLTARSF--ITCIQMISEARFPYIEGEMTRIRYNRSRSPDPSVITLENMWRL 214
QY 59 SEAHHAKNGALPKPLELVDAKGTKWIVLRVDENRDVALKY 101
DB 215 STAIQSNQGAFAASPIQLQRNRGSKFSYDVYSIPITALMY 257

RESULT 14
QBWAU4 PRELIMINARY: PRT: 305 AA.
QBWAU4 AC
DT 01-MAR-2002 (TREMBREL 20, Created)
DT 01-MAR-2002 (TREMBREL 20, Last sequence update)
DT 01-JUN-2002 (TREMBREL 21, Last annotation update)
DE Bouganin.
OS Bougainvillea spectabilis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Nyctaginaceae; Bougainvillea.
OX NCBI_TaxID=146096;
XX [1]
RN RN
RP SEQUENCE FROM N.A.
RA den Hartog M.T., Lubelli C., Boon L., Heerkens S., Ortiz Bujsse A.P.,
RA de Boer W., Stijpe F.;
RT "Cloning and expression of cDNA coding for bouganin: A type I
RT ribosome-inactivating protein from Bougainvillea spectabilis Willd.";
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF445416; AAL35962.1; -.
DR EMBL; AF445416; AAL35962.1; -.
DR InterPro; IPRO01574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; UNKNOWN_1.
SO SEQUENCE 305 AA; 34067 MW; 31505CE91962DCDB CRC64;

Query Match 33.4%; Score 188.5; DB 10; Length 305;
Best Local Similarity 43.6%; Pred. No. 4.8e-12;
Matches 41; Conservative 18; Mismatches 32; Indels 3; Gaps 2.

QY 11 AFFLLVAIQWSEARFYKFIENO-VKTNFNRAFPDPKPVINLEEKMGKISEAHINA--KN 67
DB 179 AKFLVLIIQWMSAARFKYITEVVDRLGLYSFKFNFLVNENNMGDISDAIHKSSPQC 238
QY 68 GALPKPLELVDAKGTKWIVLRVDENRDVALKY 101

```

Query Match 53.5%; Score 302; DB 10; Length 302;  
 Best Local Similarity 58.9%; Pred. No. 32e-24;  
 Matches 63; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

09  
 1 GDSFVKTAEAPFLVAIQWSEARFKYIENOVKTNNRATPPDKVINLEEKWKISDAI 60  
 176 GYAFETKEAEFLVAIQWSEARFKYIENOVKTNNRATPPDKVINLEEKWKISDAI 235

09  
 61 AHNANALPRLPLVDKGTWYLRVDEINRDVALLKYVGTCO 107  
 236 PIRNAQGVISPLNLNMGSEDEPMWYTRDEIKRYTALNFGSTCO 282

RESULT 9  
 039418 PRELIMINARY; PRT: 272 AA.

ID 039418;  
 AC 039418;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Activiral protein precursor (Ribosome-inactivating protein) (RNA N-glycosidase) (Polynucleotide:adenosine glycosidase) (EC 3.2.2.22)  
 DE (BETAVALGIN) (BVG).  
 GN RIP OR BETAVALGIN OR BVG.  
 OS Beta vulgaris (Sugar beet).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.  
 OX NCBI\_TaxID=3355;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=SEEDLING.  
 RX MEDLINE=96235141; PubMed=8666251.  
 RA Horning E., Wajant H., Jeske H., Mundry K.-W.  
 RT "Cloning of a cDNA encoding a new ribosome-inactivating protein from Beta vulgaris vulgaris (mangold).";  
 RL Gene 170:233-236(1996).  
 CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN SYNTHESIS IN VITRO. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR SUICIDE UPON INVASION BY A VIRUS.  
 CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO TYPE 1 RIP.  
 DR EMBL: X85967; CA53952.1; .  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; FALSE\_NEG.  
 KW Hydroxylase; Glycosidase; Activiral; Protein synthesis inhibitor; Toxin;  
 KW Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 272 BY SIMILARITY.  
 FT ANTI-VIRAL PROTEIN.  
 FT ACT\_SITE 196 196 BY SIMILARITY.  
 SO SEQUENCE 272 AA; 30168 MW; 77DD0917FD1FDFD CRC64;

Query Match 38.1%; Score 215; DB 10; Length 272;  
 Best Local Similarity 48.0%; Pred. No. 6e-15;  
 Matches 48; Conservative 14; Mismatches 34; Indels 4; Gaps 1;

09  
 3 DSFVKTAEAPFLVAIQWSEARFKYIENOVKTNNRATPPDKVINLEEKWKISDAI 62  
 176 DSDRREARFLVAIQWSEARFKYIENOVKTNNRATPPDKVINLEEKWKISDAI 231

09  
 63 HNAKNGALPRLPLVDKGTWYLRVDEINRDVALLKYV 102  
 232 RKAAYKVISPILVNLNMGSEDEPMWYTRDEIKRYTALNFGSTCO 271

RESULT 10

09S9E4  
 ID 09S9E4 PRELIMINARY; PRT: 258 AA.

AC 09S9E4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE rRNA - glycosidase (EC 3.2.2.22).  
 OS Gelonium multiflorum (Euphorbiaceae himalayana).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucotids I; Malpighiales; Euphorbiaceae; Gelonium.  
 OX NCBI\_TaxID=3979;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=9606751; PubMed=7553224;  
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,  
 RA Toman P.D., Cheung L.  
 RT "Amino acid sequence analysis, gene construction, cloning, and expression of gelonin, a toxin derived from Gelonium multiflorum";  
 RL J. Interferon Cytokine Res. 15:547-555(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR HSSP: P09989; IMRU.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 KW Hydroxylase; Toxin.  
 SO SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 37.7%; Score 212.5; DB 10; Length 258;  
 Best Local Similarity 44.7%; Pred. No. 1e-14;  
 Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

09  
 2 VDSFVKTAEAPFLVAIQWSEARFKYIENOVKTNNRATPPDKVINLEEKWKISDAI 61  
 152 IDNKPTREIASLLVYIQWSEARFKYIENOVKTNNRATPPDKVINLEEKWKISDAI 211

09  
 62 IH-NAKNGALPRLPLVDKGTWYLRVDEINRDVALLKYV 103  
 212 IRTSGANGMSEAVELERANGKRYTAVDQVFKILLKFDV 254

RESULT 11  
 09M5K6 PRELIMINARY; PRT: 279 AA.

ID 09M5K6;  
 AC 09M5K6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE rRNA - glycosidase (EC 3.2.2.22).  
 CN CAP30A.  
 OS Chenopodium album (Lamb's-quarters).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.  
 OX NCBI\_TaxID=3559;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Park J.S., Cho K.J., Lee S.M., Kim Y.T., Hwang Y.S.;  
 RT "A cDNA clone encoding a novel ribosome inactivating protein from Chenopodium album L.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AF228508; AAF66234.1; .  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 KW Hydroxylase; Toxin.  
 SO SEQUENCE 279 AA; 31377 MW; 2A53300E445DC952 CRC64;

```

RL Plant Mol. Biol. 43:439-450(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF141331; A032679.1; -.
DR HSSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; UNKNOWN_1.
KW Hydrolyase; Toxin.
SQ SEQUENCE 315 AA; 35728 MW; F85DE21154B5FA15 CRC64;

Query Match 77.5%; Score 437; DB 10; Length 315;
Best Local Similarity 78.9%; Pred. No. 1,1e-38;
Matches 86; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 GVDSFPVKTEAFFLLVAIQWSEARFKYIENOVKTNFNAPFPDPKVINLEEKWKIS 60
DB 179 GVDTVNKTAEFFLLVAIQWSEARFKYIENOVKTNFNAPFPDPKVINLEEKWKIS 238
DB 61 AIHNKAGALPKPELVDAAGTKWIVLRVDEINRDVALKYVNGTCOTT 109
DB 239 AIHDANKGALTKPELVNEDGTWIVLRVDEIKPVDGLNVYDGTCTT 287

RESULT 6
08S947 PRELIMINARY; PRT; 261 AA.
AC 08S947;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PAP-S1 (Fragment).
GN PAP-S1.
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RA SEQUENCE FROM N.A.
RA Honjo E., Matanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB071854; BAB86349.1; -.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 29199 MW; D88B998BEFF1F989 CRC64;

Query Match 76.1%; Score 429; DB 10; Length 261;
Best Local Similarity 78.9%; Pred. No. 6,4e-38;
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 GVDSFPVKTEAFFLLVAIQWSEARFKYIENOVKTNFNAPFPDPKVINLEEKWKIS 60
DB 153 GQDSFTEKTEAFFLLVAIQWSEARFKYIENOVKTNFNAPFPDPKVINLEEKWKIS 212
DB 61 AIHNKAGALPKPELVDAAGTKWIVLRVDEINRDVALKYVNGTCOTT 109
DB 213 AIHNSKNGALPKPELVDAAGTKWIVLRVDEIKPVDGLNVYDGTCTT 261

RESULT 7
09ATB3 PRELIMINARY; PRT; 237 AA.
AC 09ATB3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22) (Fragment).
SQ SEQUENCE 302 AA; 33955 MW; B0561C3910C2E6A2 CRC64;

```

```

GN MPAP.
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RA SEQUENCE FROM N.A.
RA Chen D., Wang X., Zhou G.;
RT "Pokeweed antiviral protein gene/partical cds."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF338910; AAK21951.1; -.
DR HSSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
KW Hydrolyase; Toxin.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 26534 MW; FE4ADCEE03464783 CRC64;

Query Match 62.9%; Score 355; DB 10; Length 237;
Best Local Similarity 83.3%; Pred. No. 4,9e-30;
Matches 70; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 GVDSFPVKTEAFFLLVAIQWSEARFKYIENOVKTNFNAPFPDPKVINLEEKWKIS 60
DB 154 GVSFTEKTEAFFLLVAIQWSEARFKYIENOVKTNFNAPFPDPKVINLEEKWKIS 213
DB 61 AIHNKAGALPKPELVDAAGTKW 84
DB 214 AIHANKNGVLPKPELVDAAGAKW 237

RESULT 8
P93077 PRELIMINARY; PRT; 302 AA.
AC P93077;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
GN RIP.
OS Clerodendrum aculeatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiales; Clerodendrum.
OX NCBI_TaxID=54208;
RN [1]
RA SEQUENCE FROM N.A.
RA TISSUE-LEAF.
RA MEDLINE=97238481; PubMed=9132066;
RA Kumar D., Verma H.N., Tuteja N., Tewari K.K.;
RT "Cloning and characterisation of a gene encoding an antiviral protein
RT from Clerodendrum aculeatum L."
RL Plant Mol. Biol. 33:745-751(1997).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: X96474; CAA65328.1; -.
DR EMBL: X96583; CAA65402.1; -.
DR HSSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
KW Glycosidase; Hydrolyase; Toxin.
SQ SEQUENCE 302 AA; 33955 MW; B0561C3910C2E6A2 CRC64;

```

[illegible]

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 15.7673 Seconds

(without alignments)  
1424.413 Million cell updates/sec

Title: US-09-978-274A-4\_COPY\_155\_263

Perfect score: 564  
Sequence: 1 GVDSFPYKTEAFLLVAIQM.....DEINRDVALLKYNCTCOT 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_RVIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564	100.0	314	10	P93444
2	559	99.1	362	10	O8S946
3	449	79.6	313	10	O941G8
4	438	77.7	339	10	O8RYA4
5	437	77.5	315	10	O9XFF8
6	429	76.1	261	10	O8S947
7	355	62.9	237	10	O9ATB3
8	302	53.5	302	10	P93077
9	215	38.1	272	10	O93418
10	212.5	37.7	258	10	O9S9E4
11	207.5	35.0	279	10	O9S9E6
12	197.5	35.0	279	10	O9AUE3
13	192	34.0	541	10	O41174
14	188.5	33.4	305	10	O8W4U4
15	170.5	30.2	294	10	O93Y65
16	170.5	30.2	294	10	O93Y64

17	154.5	27.4	294	10	O93Y66	O93Y66 dianthus ch
18	149	26.4	289	10	P93261	P93261 mesembryant
19	147.5	26.2	549	10	O9EV22	O9EV22 cinanomom
20	147.5	26.2	580	10	O94BW3	O94BW3 cinanomom
21	147.5	26.2	581	10	O94BW5	O94BW5 cinanomom
22	146.5	26.0	270	10	O9SA05	O9SA05 amarantus
23	146.5	26.0	319	10	O8VWY2	O8VWY2 spinacia ol
24	146	25.9	289	10	O94KE4	O94KE4 trichosan
25	145	25.7	247	10	O9LRE3	O9LRE3 trichosan
26	145	25.7	289	10	O41216	O41216 trichosan
27	145	25.7	270	10	O8SA43	O8SA43 abrus preca
28	144	25.5	270	10	O41611	O41611 trichosan
29	143.5	25.4	279	10	O9ZRT5	O9ZRT5 amarantus
30	143.5	25.4	284	10	O96322	O96322 amarantus
31	143.5	25.4	580	10	O94BW4	O94BW4 cinanomom
32	138	24.5	293	10	O8VYU0	O8VYU0 jatropa cu
33	137.5	24.4	251	10	O48859	O48859 amarantus
34	137.5	24.4	278	10	O00980	O00980 luffa cylin
35	137	24.3	286	10	O9FUV7	O9FUV7 momordica c
36	135	23.9	252	10	O38761	O38761 abrus preca
37	134	23.8	565	10	O04071	O04071 sambucus n
38	134	23.8	566	10	O04072	O04072 sambucus n
39	133.5	23.7	604	10	O9M654	O9M654 polygonat
40	133	23.6	293	10	O8S452	O8S452 jatropa cu
41	133	23.6	547	10	O9M6E9	O9M6E9 abrus preca
42	132.5	23.5	570	10	O22415	O22415 sambucus n
43	132.5	23.5	603	10	O9M653	O9M653 polygonat
44	132	23.4	264	10	O9F5H2	O9F5H2 momordica c
45	132	23.4	286	10	O41257	O41257 momordica c

## ALIGNMENTS

RESULT 1  
P93444 PRELIMINARY; PRT; 314 AA.  
ID P93444  
AC P93444  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE rRNA - glycosidase precursor (EC 3.2.2.22).  
GN PAP-S.  
OS Phytolacca americana (Common pokeweed) (Virginiaian pokeweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SEED;  
RX MEDLINE=97263479; PubMed=9109394;  
RA Poyet J.L., Hoeveler A.;  
RT "cDNA cloning of the gene encoding the Antiviral protein from the  
RT seeds of Phytolacca americana and its expression in E.coli.";  
RL FEBS Lett. 406:97-100(1997).  
CC -|- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
CC EMBL: X98079; CA66702.1;  
CC HSSP: O03464; IAPA.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.1.  
DR PRINTS: PR00396; SHIGA\_RICIN.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
DR Hydrolase; Signal; Toxin.  
FT SIGNAL 1 24  
FT CHAIN 25 314 POTENTIAL.  
SQ SEQUENCE 314 AA; 35323 MW; A89E3CE57789F9E CRC64;  
Query Match 100.0%; Score 564; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 2.7e-52;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 23 VNTIIVNGSTTISKYATFLNDRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKK 82  
QY 62 TITLMLRRNNLYVWGSDPENGKCRHYIENDISTERTDYENTLSCSSSSRVAMSTINYN 121  
Db 83 TITLMLRRNNLYVWGSDPFTNCRHYIENDISGTERTDQDETLCPNANRVSKNINFD 142  
QY 122 SLVPTMEKKAEVNSRNOVOLGIQILSSDICKISGVDSFPVYTEAFLLVAIQWSEARF 181  
Db 143 SRYPTELESKAGVKSRSOVOLGIQILDSNICKISGVMSFTEKTEAFLLVAIQWSEARF 202  
QY 182 KYIENOVKTNNRAFNPDPRVYNLEEKWKISEAIHNKAGALPKPLELVDAGKTKWIVL 241  
Db 203 KYIENOVKTNNRAFNPNPKVNLQETWGIKISTAIHDAKNGLPKPLELVDASGAKWIVL 262  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
Db 263 RVDEIKPDVALLNIVGSCOTT 284

## RESULT 15

US-08-500-694-2

Sequence 2, Application US/08500694  
Patent No. 5880329

GENERAL INFORMATION:

APPLICANT: Tumer, Nilgun E.

TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lerner, David, Litlenberg, Krumholz &amp; Mentlik

STREET: 600 South Avenue West

CITY: Westfield

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/500,694

FILING DATE: 11-JUL-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.

REFERENCE/DOCKET NUMBER: OCIRS 3.0-039

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000

TELEFAX: 908-654-7866

TELEX: 139-125

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-500-694-2

Query Match 77.4%; Score 1050; DB 2; Length 313;

Best Local Similarity 76.3%; Pred. No. 5.4e-100;

Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

QY 2 INTITDAGNATINKYATFMESLRNOAKDKLKCYGIPMLPDNTSTPKYLLVLOGANLK 61  
Db 23 VNTIIVNGSTTISKYATFLNDRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKK 82  
QY 62 TITLMLRRNNLYVWGSDPENGKCRHYIENDISTERTDYENTLSCSSSSRVAMSTINYN 121  
Db 83 TITLMLRRNNLYVWGSDPFTNCRHYIENDISGTERTDQDETLCPNANRVSKNINFD 142  
QY 122 SLVPTMEKKAEVNSRNOVOLGIQILSSDICKISGVDSFPVYTEAFLLVAIQWSEARF 181  
Db 143 SRYPTELESKAGVKSRSOVOLGIQILDSNICKISGVMSFTEKTEAFLLVAIQWSEARF 202  
QY 182 KYIENOVKTNNRAFNPDPRVYNLEEKWKISEAIHNKAGALPKPLELVDAGKTKWIVL 241  
Db 203 KYIENOVKTNNRAFNPNPKVNLQETWGIKISTAIHDAKNGLPKPLELVDASGAKWIVL 262  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
Db 263 RVDEIKPDVALLNIVGSCOTT 284

Db 143 SRYPTELESKAGVKSRSOVOLGIQILDSNICKISGVMSFTEKTEAFLLVAIQWSEARF 202  
QY 182 KYIENOVKTNNRAFNPDPRVYNLEEKWKISEAIHNKAGALPKPLELVDAGKTKWIVL 241  
Db 203 KYIENOVKTNNRAFNPNPKVNLQETWGIKISTAIHDAKNGLPKPLELVDASGAKWIVL 262  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
Db 263 RVDEIKPDVALLNIVGSCOTT 284

Search completed: July 2, 2003, 11:40:28  
Job time : 18.9544 secs



Matches 216; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYIPMLPDTNSTPKYLLVKGANLK 61  
Db 1 INTTFDAGNATINKYATFEMESLRNEADPSLKCYPMLPNTNTPKYVLEVGSKRK 82  
QY 62 TITMLRRNNLYVGYSDPFNGKCRHIFNDISTERTDVENTLSCSSSRVMSINYN 121  
Db 61 TITMLRRNNLYVGYSDPDYD-NKCRHIFNDIKETGTEVDVENTLCPSSNPRVAKPINYN 119  
QY 122 SLPTMEKKAEVNSRNOVQGIQLSSDICKISGVDSFPKTEAFELVAIQVSEARF 181  
Db 120 GYPTLEKKAGVTSNEVOLLGIISSKIGKISGGSFTKEIEADFLVAIQVSEARF 179  
QY 182 KYIENQVKTNFNRAFYDDPKVINLEEKWKISEAHNAKNGALPKPLEVDAGTKWIVL 241  
Db 180 KYIENQVKTNFNRAFYDDPKVLDLENNMGKISTAHNSKNGALPKPLEVDAGTKWIVL 239  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
Db 240 RVDEIKPDVGLLNYVNGTCOAT 261

## RESULT 13

US-08-373-858-2  
Sequence 2, Application US/08373858  
Patent No. 563135

## GENERAL INFORMATION:

APPLICANT: Kim, Man-Keun  
APPLICANT: Lee, Kwan-Ho  
APPLICANT: Na, Byeong-Kook  
APPLICANT: Jeong, Han-Seung  
APPLICANT: Choi, Kyu-Wan  
APPLICANT: Moon, Young-Ho  
APPLICANT: Jeon, Hong-Seob  
TITLE OF INVENTION: Expression Vector for Phytoacta  
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10022-7513

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,858  
FILING DATE: 18-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Peter  
REGISTRATION NUMBER: 25,351  
REFERENCE/DOCKET NUMBER: 0136/17986-US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7770  
TELEFAX: 212-753-6237  
TELEX: 236687

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Phytoacta americana

TISSUE TYPE: Leaf  
US-08-373-858-2

Query Match  
Best Local Similarity 77.4%; Score 1050; DB 1; Length 313;  
Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYIPMLPDTNSTPKYLLVKGANLK 61  
Db 23 VNTLIYVNGSTTISKYATFELNDLRNEADPSLKCYPMLPNTNTPKYVLEVGSKRK 82  
QY 62 TITMLRRNNLYVGYSDPFNGKCRHIFNDISTERTDVENTLSCSSSRVMSINYN 121  
Db 83 TITMLRRNNLYVGYSDPFNGKCRHIFNDISTERTDVENTLSCSSSRVMSINYN 142  
QY 122 SLPTMEKKAEVNSRNOVQGIQLSSDICKISGVDSFPKTEAFELVAIQVSEARF 181  
Db 143 SRPTLESKAGVKSRSOVQGIQLSDINICKISGVMSFTKTEAFELVAIQVSEARF 202  
QY 182 KYIENQVKTNFNRAFYDDPKVINLEEKWKISEAHNAKNGALPKPLEVDAGTKWIVL 241  
Db 203 KYIENQVKTNFNRAFYDDPKVNLQETWCKISTAHNAKNGALPKPLEVDAGTKWIVL 262  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
Db 263 RVDEIKPDVALLNYVNGTCOTT 284

## RESULT 14

US-08-500-611-2  
Sequence 2, Application US/08500611  
Patent No. 5756322

## GENERAL INFORMATION:

APPLICANT: Turner, Nilgun E.  
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,611  
FILING DATE: 11-JUL-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
TELEX: 139-125

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-500-611-2

Query Match  
Best Local Similarity 77.4%; Score 1050; DB 1; Length 313;  
Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYIPMLPDTNSTPKYLLVKGANLK 61  
Db 1 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYIPMLPDTNSTPKYLLVKGANLK 61



OY 182 KYIENOVKTNFNRFPYDPKVINLEEKWKISEAIIHNAKNGALPKPLELVDAKGTWIVL 241  
DB 180 KYIENOVKTNFNRFPSPNDKVLDEENMGKISTAIHNSKNGALPKPLELVDAKGTWIVL 239  
OY 242 RVDEINRDVALLKYVNGTCOTT 263  
DB 240 RVDEIKPDVGLLVYNGTCOAT 261

## RESULT 9

US-07-901-707-9  
; Sequence 9, Application US/07901707  
; Patent No. 5376546  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Steve F.  
; APPLICANT: Lane, Julie A.  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/901,707  
; FILING DATE: 19920619  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5376546and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27129/30910  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-5750  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-901-707-9

Query Match 80.3%; Score 1089.5; DB 1; Length 261;  
Best Local Similarity 82.4%; Pred. No. 3.6e-104;  
Matches 216; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

OY 2 INTITFDAGNATINKYATFMESLRNQAADPKLKCIGIMLPDNTSPRYLLVLOGANLK 61  
DB 1 INTITFDAGNATINKYATFMESLRNQAADPKLKCIGIMLPDNTSPRYLLVLOGANLK 60  
OY 62 TITLMLRRNNLYVMGSDPFGNKKRYHIFNDITSTERTDVENTLCSSSSSRVAMSIYNV 121  
DB 61 TITLMLRRNNLYVMGSDPFGNKKRYHIFNDITSTERTDVENTLCSSSSSRVAMSIYNV 119  
OY 122 SLVPTMEKKAVNRRNOVAGIOTLSSDICKISGVDSFPVKTFAFLVLAIOVSEARF 181  
DB 121 SLVPTMEKKAVNRRNOVAGIOTLSSDICKISGVDSFPVKTFAFLVLAIOVSEARF 179

DB 120 GLVPTLEKKAGVTSRNEVOAGIOTLSSDICKISGVDSFPVKTFAFLVLAIOVSEARF 179  
OY 182 KYIENOVKTNFNRFPYDPKVINLEEKWKISEAIIHNAKNGALPKPLELVDAKGTWIVL 241  
DB 180 KYIENOVKTNFNRFPSPNDKVLDEENMGKISTAIHNSKNGALPKPLELVDAKGTWIVL 239  
OY 242 RVDEINRDVALLKYVNGTCOTT 263  
DB 240 RVDEIKPDVGLLVYNGTCOAT 261

## RESULT 10

US-07-988-430-9  
; Sequence 9, Application US/07988430  
; Patent No. 5416202  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,430  
; FILING DATE: 19921209  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5416202and, Greta E.  
; REGISTRATION NUMBER: 35302  
; REFERENCE/DOCKET NUMBER: 31133  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-988-430-9

Query Match 80.3%; Score 1089.5; DB 1; Length 261;  
Best Local Similarity 82.4%; Pred. No. 3.6e-104;  
Matches 216; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

OY 2 INTITFDAGNATINKYATFMESLRNQAADPKLKCIGIMLPDNTSPRYLLVLOGANLK 61  
DB 1 INTITFDAGNATINKYATFMESLRNQAADPKLKCIGIMLPDNTSPRYLLVLOGANLK 60  
OY 62 TITLMLRRNNLYVMGSDPFGNKKRYHIFNDITSTERTDVENTLCSSSSSRVAMSIYNV 121  
DB 61 TITLMLRRNNLYVMGSDPFGNKKRYHIFNDITSTERTDVENTLCSSSSSRVAMSIYNV 119

COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-9

Query Match 80.8%; Score 1096.5; DB 4; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6,8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNOAKDPKLCYGIPLPDTNSTPKYLLVKGANLK 61  
|||||  
DB 1 INTITFDAGNATINKATFMESLRNEAKDPSLKYGIPLPDTNSTIKYLLVKGASLK 60  
|||||  
QY 62 TITLMLRRNNLYVGYSDPFNGKCRHYHFNIDITSTERDVENTLSSSSSRVAMSINN 121  
|||||  
DB 61 TITLMLRRNNLYVGYSDPYD-NKCRHYHFNIDIKTEYSDEVENTLCPSSNPRVAKPIYNN 119  
|||||  
QY 122 SLVPTMEKRAEVNSRNOVOLGIOLISSDICKISGVSPFKTAEFLVAIQVSEARF 181  
|||||  
DB 120 GLVPTLEKRAGVTSRNEVOLGIOLISSDICKISGVGFTEKLEADFLVAIQVSEARF 179  
|||||  
QY 182 KYTENOVKTNFNFAFPDPKVINLEEKMKISEAHINAKGALPKPLEVDATKWIYV 241  
|||||  
DB 180 KYTENOVKTNFNDFSPNDKVIDLEENWGKISTAHNSKNGALPKPLELNADGTWIVL 239  
|||||  
QY 242 RVDEINRDVALKYVNGTCQT 263  
|||||  
DB 240 RVDEIKRPDVGLLYVNGTCQAT 261  
|||||

RESULT 8  
US-09-610-838-9  
; Sequence 9, Application US/09610838  
; Patent No. 6376217

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studilka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,838  
FILING DATE: 06-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-610-838-9

Query Match 80.8%; Score 1096.5; DB 4; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6,8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNOAKDPKLCYGIPLPDTNSTPKYLLVKGANLK 61  
|||||  
DB 1 INTITFDAGNATINKATFMESLRNEAKDPSLKYGIPLPDTNSTIKYLLVKGASLK 60  
|||||  
QY 62 TITLMLRRNNLYVGYSDPFNGKCRHYHFNIDITSTERDVENTLSSSSSRVAMSINN 121  
|||||  
DB 61 TITLMLRRNNLYVGYSDPYD-NKCRHYHFNIDIKTEYSDEVENTLCPSSNPRVAKPIYNN 119  
|||||  
QY 122 SLVPTMEKRAEVNSRNOVOLGIOLISSDICKISGVSPFKTAEFLVAIQVSEARF 181  
|||||  
DB 120 GLVPTLEKRAGVTSRNEVOLGIOLISSDICKISGVGFTEKLEADFLVAIQVSEARF 179  
|||||

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-9

Query Match 80.8%; Score 1096.5; DB 2; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNQAOKPKLCYCIPLPDTNSTPKYLVLKLGANLK 61  
DB 1 INTITFDAGNATINKATFMESLRNQAOKPKLCYCIPLPDTNSTPKYLVLKLGANLK 60  
QY 62 TTTLMLRRNNLYVMGYSDPFNGKCRHYIFNDITSTERTDVENTLCCSSSSRVAMSIYN 121  
DB 61 TTTLMLRRNNLYVMGYSDPYD-NKCRHYIFNDIKGTEYSDVENTLCPSSNPRVAKPIYN 119  
QY 122 SLVPTMEKAEVNSRQVGLGIQLISSDGIKISGVDSFPVKTEAFPLVAIOMVSEARF 181  
DB 120 GLVPTLEKKAAGVTSRNEVGLGIQLISSDGIKISGVDSFTEKTEADFLVAIOMVSEARF 179  
QY 182 KYIENQVKTNFNRAFPDPKVINLEEKMGKISEAITHNKNKALPKPLVDAKGTWIVL 241  
DB 180 KYIENQVKTNFNRPDSFNDKVLDEENMGKISTAIHNSKNKALPKPLKADGTWIVL 239  
QY 242 RVDEINRDVALKLVNGTCQTT 263  
DB 240 RVDEIKPDVGLLVNGTCQAT 261

## RESULT 6

Sequence 9, Application US/08839765  
Patent No. 6146631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-839-765-9

Query Match 80.8%; Score 1096.5; DB 4; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNQAOKPKLCYCIPLPDTNSTPKYLVLKLGANLK 61  
DB 1 INTITFDAGNATINKATFMESLRNQAOKPKLCYCIPLPDTNSTPKYLVLKLGANLK 60  
QY 62 TTTLMLRRNNLYVMGYSDPFNGKCRHYIFNDITSTERTDVENTLCCSSSSRVAMSIYN 121  
DB 61 TTTLMLRRNNLYVMGYSDPYD-NKCRHYIFNDIKGTEYSDVENTLCPSSNPRVAKPIYN 119  
QY 122 SLVPTMEKAEVNSRQVGLGIQLISSDGIKISGVDSFPVKTEAFPLVAIOMVSEARF 181  
DB 120 GLVPTLEKKAAGVTSRNEVGLGIQLISSDGIKISGVDSFTEKTEADFLVAIOMVSEARF 179  
QY 182 KYIENQVKTNFNRAFPDPKVINLEEKMGKISEAITHNKNKALPKPLVDAKGTWIVL 241  
DB 180 KYIENQVKTNFNRPDSFNDKVLDEENMGKISTAIHNSKNKALPKPLKADGTWIVL 239  
QY 242 RVDEINRDVALKLVNGTCQTT 263  
DB 240 RVDEIKPDVGLLVNGTCQAT 261

## RESULT 7

US-09-136-389-9  
Sequence 9, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois

US-08-488-113B-9

Query Match 80.8%; Score 1096.5; DB 1; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFMSLRNQAADPKLCYGIPLPDPTNSTPKYLLVKGLOGANLK 61  
1 INTTFDAGNATINKYATFMSLRNQAADPKLCYGIPLPDPTNSTPKYLLVKGLOGANLK 60  
DB 61 TITLMRRNNLYVMGYSDPFGNKKCRHIFNDITSTERTDVENTLCSSSSSRVAMSTYN 119  
QY 62 TITLMRRNNLYVMGYSDPFGNKKCRHIFNDITSTERTDVENTLCSSSSSRVAMSTYN 121  
119  
DB 122 SLVPTMEKKAENVNSNOVQIGIQLISSDICKISGVDSFPVKTTEAFLLVAIOMVSEARF 181  
120 GLYPLEKKAGVTSRNEVQIGIQLISSDICKISGVDSFTEKIEADFLVAIOMVSEARF 179  
QY 182 KYIENOVNTNFRNFAFPDPKVINLEEKWKISEAIIHNKNGALPKPELVDAKGTWIVL 241  
180 KYIENOVNTNFRNFAFPDPKVINLEEKWKISEAIIHNKNGALPKPELVDAKGTWIVL 239  
DB 242 RVDEINRDVALLKTVNGTCQTT 263  
240 RVDEIKPDVGLNLYNGTCQAT 261

## RESULT 4

US-08-477-484B-9

Sequence 9, Application US/08477484B  
Patent No. 5756699

## GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-477-484B-9

Query Match 80.8%; Score 1096.5; DB 1; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFMSLRNQAADPKLCYGIPLPDPTNSTPKYLLVKGLOGANLK 61  
1 INTTFDAGNATINKYATFMSLRNQAADPKLCYGIPLPDPTNSTPKYLLVKGLOGANLK 60  
DB 61 TITLMRRNNLYVMGYSDPFGNKKCRHIFNDITSTERTDVENTLCSSSSSRVAMSTYN 119  
QY 62 TITLMRRNNLYVMGYSDPFGNKKCRHIFNDITSTERTDVENTLCSSSSSRVAMSTYN 121  
119  
DB 122 SLVPTMEKKAENVNSNOVQIGIQLISSDICKISGVDSFPVKTTEAFLLVAIOMVSEARF 181  
120 GLYPLEKKAGVTSRNEVQIGIQLISSDICKISGVDSFTEKIEADFLVAIOMVSEARF 179  
QY 182 KYIENOVNTNFRNFAFPDPKVINLEEKWKISEAIIHNKNGALPKPELVDAKGTWIVL 241  
180 KYIENOVNTNFRNFAFPDPKVINLEEKWKISEAIIHNKNGALPKPELVDAKGTWIVL 239  
DB 242 RVDEINRDVALLKTVNGTCQTT 263  
240 RVDEIKPDVGLNLYNGTCQAT 261

## RESULT 5

US-08-646-360-9

Sequence 9, Application US/08646360  
Patent No. 5837491

## GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992

QY 62 TITLMBRNLLYMGSDPFGNKKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121  
Db 61 TITLMBRNLLYMGSDPYD-NKCRHYHFNIDKGTESDVENTLCPSSNPRAKPINYN 119  
QY 122 SLVPTMEKAEVSRNOVOGLIOILSSDICKISGVDSFPVKTAEFLVAIOMVSEARF 181  
Db 120 GLVPTLEKKAAGVSRNEVOGLIOILSSDICKISGVDSFTEKIEAKFLVAIOMVSEARF 179  
QY 182 KYIENOVKTNFNRAPYDPKVINLEEKMGKISEAIHNANKGALPKPLELDVAKGTWIVL 241  
Db 180 KYIENOVKTNFNRDPSFNKVDLDEBNMGKISTAHNSKNGALPKPLELDVAKGTWIVL 239  
QY 242 RVDEINRDVALLKYNGTCQT 263  
Db 240 RVDEIKPDVGLNLYNGTCQAT 261

RESULT 2  
US-08-485-286-79

; Sequence 79, Application US/08485286  
; Patent No. 5646026  
; Patent No. 5646026 5646119  
; GENERAL INFORMATION:  
; APPLICANT: WALSH, TERENCE A  
; APPLICANT: HEY, TIMOTHY D  
; APPLICANT: MORGAN, ALICE ER  
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANDREA T. BORUCKI  
; STREET: 9330 ZIONSVILLE ROAD  
; CITY: INDIANAPOLIS  
; STATE: IN  
; COUNTRY: US  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,286  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/378761  
; FILING DATE: 26-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BORUCKI, ANDREA T  
; REGISTRATION NUMBER: 33651  
; REFERENCE/DOCKET NUMBER: 38272B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 337-4846  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-286-79

Query Match 80.8%; Score 1096.5; DB 1; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6,8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKYATFMESLRNQADPKLKCYGIPMLPTNSPYLLVWKLOGANLK 61  
Db 1 INTITFDAGNATINKYATFMESLRNQADPKLKCYGIPMLPTNSPYLLVWKLOGASLK 60

QY 62 TITLMBRNLLYMGSDPFGNKKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121  
Db 61 TITLMBRNLLYMGSDPYD-NKCRHYHFNIDKGTESDVENTLCPSSNPRAKPINYN 119  
QY 122 SLVPTMEKAEVSRNOVOGLIOILSSDICKISGVDSFPVKTAEFLVAIOMVSEARF 181  
Db 120 GLVPTLEKKAAGVSRNEVOGLIOILSSDICKISGVDSFTEKIEAKFLVAIOMVSEARF 179  
QY 182 KYIENOVKTNFNRAPYDPKVINLEEKMGKISEAIHNANKGALPKPLELDVAKGTWIVL 241  
Db 180 KYIENOVKTNFNRDPSFNKVDLDEBNMGKISTAHNSKNGALPKPLELDVAKGTWIVL 239  
QY 242 RVDEINRDVALLKYNGTCQT 263  
Db 240 RVDEIKPDVGLNLYNGTCQAT 261

RESULT 3  
US-08-488-113B-9

; Sequence 9, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELETYPE: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 16.9544 Seconds

(Without alignments)  
456,414 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357  
1 MINTIFDGNATINKYATF.....DEINRDVALLKYNVGTCTT 263

Sequence: BLOSOM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA:\*  
1: /cgn2\_6/ptodata/1/1aa/55A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/55B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/55C.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/55D.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/55E.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/55F.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1096.5	80.8	261	1 US-08-378-761A-79	Sequence 79, Appl
2	1096.5	80.8	261	1 US-08-485-286-79	Sequence 79, Appl
3	1096.5	80.8	261	1 US-08-488-113B-9	Sequence 9, Appl
4	1096.5	80.8	261	1 US-08-477-484B-9	Sequence 9, Appl
5	1096.5	80.8	261	2 US-08-646-360-9	Sequence 9, Appl
6	1096.5	80.8	261	4 US-08-839-765-9	Sequence 9, Appl
7	1096.5	80.8	261	4 US-09-136-389-9	Sequence 9, Appl
8	1096.5	80.8	261	4 US-09-610-838-9	Sequence 9, Appl
9	1089.5	80.3	261	1 US-07-901-707-9	Sequence 9, Appl
10	1089.5	80.3	261	1 US-07-988-430-9	Sequence 9, Appl
11	1089.5	80.3	261	1 US-08-425-336-9	Sequence 9, Appl
12	1089.5	80.3	261	5 PCT-US92-09487-9	Sequence 9, Appl
13	1050	77.4	313	1 US-08-373-858-2	Sequence 2, Appl
14	1050	77.4	313	1 US-08-500-611-2	Sequence 2, Appl
15	1050	77.4	313	1 US-08-500-694-2	Sequence 2, Appl
16	1050	77.4	313	4 US-09-005-273-2	Sequence 2, Appl
17	1050	77.4	313	5 PCT-US96-11546-2	Sequence 2, Appl
18	1047	77.2	313	4 US-08-501-253A-2	Sequence 2, Appl
19	1042	76.8	313	4 US-09-005-273-4	Sequence 4, Appl
20	862.5	63.6	305	1 US-08-138-636-2	Sequence 2, Appl
21	862.5	63.6	305	1 US-08-319-622A-2	Sequence 2, Appl
22	862.5	63.6	305	1 US-08-471-564-2	Sequence 2, Appl
23	342	25.2	259	1 US-07-901-707-10	Sequence 10, Appl
24	342	25.2	259	1 US-07-988-430-10	Sequence 10, Appl
25	342	25.2	259	1 US-08-425-336-10	Sequence 10, Appl
26	342	25.2	259	1 US-08-488-113B-10	Sequence 10, Appl
27	342	25.2	259	1 US-08-477-484B-10	Sequence 10, Appl

28	342	25.2	259	2 US-08-646-360-10	Sequence 10, Appl
29	342	25.2	259	4 US-08-839-765-10	Sequence 10, Appl
30	342	25.2	259	4 US-09-136-389-10	Sequence 10, Appl
31	342	25.2	259	4 US-09-610-838-10	Sequence 10, Appl
32	342	25.2	259	5 PCT-US92-09487-10	Sequence 10, Appl
33	342	25.2	260	1 US-08-378-761A-72	Sequence 72, Appl
34	342	25.2	260	1 US-08-485-286-72	Sequence 72, Appl
35	322.5	23.8	258	5 PCT-US91-05766-2	Sequence 2, Appl
36	319.5	23.5	292	1 US-08-378-761A-81	Sequence 81, Appl
37	319.5	23.5	292	1 US-08-485-286-81	Sequence 81, Appl
38	316	23.3	251	1 US-08-425-336-108	Sequence 108, App
39	316	23.3	251	1 US-08-488-113B-108	Sequence 108, App
40	316	23.3	251	1 US-08-477-484B-108	Sequence 108, App
41	316	23.3	251	2 US-08-646-360-108	Sequence 108, App
42	316	23.3	251	4 US-08-839-765-108	Sequence 108, App
43	316	23.3	251	4 US-09-136-389-108	Sequence 108, App
44	316	23.3	251	4 US-09-610-838-108	Sequence 108, App
45	314	23.1	251	1 US-08-425-336-101	Sequence 101, App

## ALIGNMENTS

RESULT 1  
US-08-378-761A-79  
Sequence 79, Application US/08378761A  
Patent No. 563584  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-79

Query Match 80.8%; Score 1096.5; DB 1; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

2 INTTFPAGNATINKYATFMESLRNQAADKRLKCYGIPMLPDNTPKRYLLVLOGANLK 61  
1 INTTFPAGNATINKYATFMESLRNQAADKRLKCYGIPMLPDNTPKRYLLVLOGANLK 60



Db 189 AHDAKNGVLPKPLELVDSAGAKWIVLRVDEIKPDVALLNYYGSGSCOTT 237

Search completed: July 2, 2003, 11:39:42  
Job time : 21.0629 secs

Db 127 GVWSFEKTEAEFLVLAIQWSEARFYIENQVNTNENRANPNPKVLINQETMGRIST 186

Qy 62 AIHNAKNGALPKPLELYDAKTKKTVLVNDENRVALTKVNGTCQT 110

Db 187 AIHDANGVLPKPLELYDASGAKWVLYERDEIKPVALALNIVGSCQT 235

RESULT 14	
AAW14243	
ID AAW14243	standard; protein; 236 AA

AC	AAW14243;	
XX		
DT	25-JUN-1997	(first entry)

DE Mature pokeweed antiviral protein deletion variant (27-262).

KW Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.

OS Phytolacca americana.

PN W09703183-A1.

PD 30-JAN-1997.

11-JUL-1996; 96WO-US11546

PR 11-JUL-1995; 95US-0500694.

XX 11-00L-1990; 9505-0300611-  
XX

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY

Tumer NE;

DR WPI; 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral

PT and anti-fungal activity in plants and have reduced phytotoxicity.

PS Claim 14; -; 64pp; English.

CC ProteinsAAW1163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW1465-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenosine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.

SQ Sequence 236 AA;

Query Match	79.8%;	Score 454;	DB 18;	Length 236;
Best Local Similarity	82.6%;	Pred. No. 1.3e-46;		
Matches 90;	Conservative 5;	Mismatches 14;	Indels 0;	Gaps 0

OY            2 GVDSEPVKTEAFLFLVAIQVSEARFKYIEQVKTNENRAPPDPKYINLEEKWKISE 61  
              || || ||| ||||||||||||||||||| : |||:|| | ||||  
Db          128 GVMSFTEKEAEFLFLVAIQVSEARFKYIEQVKTNPNRRAPNPKVLNLQETWGIIST 18

```
QY      62 AIHNAKAGALPKPLELVDAKGKTWIVLRVDEIRNDVALLLKYVNGTCQT 110
        |||::||| |||||||| | ||||||||| |||| | | :|||
Db     188 AIHDANKNLPKPLELVDASGAKWIVLRVDEIRPDVALLNVGGSCQT 236
```

RESULT 15  
AAW14242  
ID AAW14242 standard; protein; 237 AA

AC AAW14242:

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (26-262).

KW Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;  
 KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KW bacterium.

Phytolacca americana

PN WO9703183-A1

PD 30-JAN-1997

11-JUL-1996; 96WO-US11546

AA  
PR 11-JUL-1995; 95US-0500694

XX  
XX  
XX

9305-0300611  
666T-1993;  
9305-0300611

FA (KOLF) ONLY KUIGERS STATE NEW JERSEY  
XX

JUNCEY ME,  
XX

XX  
XX

NEW, 1971 115040/11

PT and anti-fungal activity in plants and have reduced phytotoxicity

PS Claim 14; -; 64pp; English.

CC Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongatio  
CC factor-2 binding thus blocking protein translation. The PAP mutants ca  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.

AA	Sequence	237	AA
SQ			

Query Match	79.88;	Score 454;	DB 18;	Length 237;
Best Local Similarity	82.6%;	Pred. No. 1.3e-46;		
Matches 90:	Conservative	5;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY 2 GVDSPVKTEAFLFLVAIQMWSEARFKYLENQVKTNFNRAPYPDPKVTINLEKWKGTISE 61  
II II IIII IIII IIII IIII IIII IIII IIII : : : : :  
Db 129 GVMSFTEKEAEFLFLVAIQMWSEARFKYLENQVKTNFNRAPNPYPYLNIQETWKGKIST 188

62 AIHNAKNGALPKPELVDAKGTKWIVLRVDEINRDVALLKVVNGTCOTT 110



XX Sequence 231 AA;  
SO Query Match 79.8%; Score 454; DB 18; Length 231;  
Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90: Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSFPKTEAFLLVAIQWSEARFKYIENQVKTNFNRAFPDPKVINLEEKWKISE 61  
DB 123 GVMSFTEKTEAFLLVAIQWSEARFKYIENQVKTNFNRAFPDPKVINLEETWKGIST 182  
OY 62 AIHAKNGALPKPELVDAKGTKWIVLRVDEINRDVALLKRVNGTCOTT 110  
DB 183 AIHDAKNGVLPKPELVDAKGAKWIVLRVDEIKPDPVALLNVGSCOTT 231

RESULT 10  
AAW14247  
ID AAW14247 standard; protein: 232 AA.  
AC AAW14247;  
XX 25-JUN-1997 (first entry)  
DT  
XX Mature pokeweed antiviral protein deletion variant (31-262).  
DE  
XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
XX  
XX Phytoacca americana.  
OS  
XX W09703183-A1.  
PN  
XX 30-JAN-1997.  
PD  
XX 11-JUL-1996; 96WO-US11546.  
PF  
XX 11-JUL-1995; 95US-0500694.  
PR 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PA  
XX Tuner NE;  
PI  
XX WPI: 1997-119040/11.  
DR  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
XX Claim 14: -: 6app; English.  
PS  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SQ Sequence 232 AA;

XX Query Match 79.8%; Score 454; DB 18; Length 232;  
SO Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90: Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSFPKTEAFLLVAIQWSEARFKYIENQVKTNFNRAFPDPKVINLEEKWKISE 61  
DB 124 GVMSFTEKTEAFLLVAIQWSEARFKYIENQVKTNFNRAFPDPKVINLEETWKGIST 183  
OY 62 AIHAKNGALPKPELVDAKGTKWIVLRVDEINRDVALLKRVNGTCOTT 110  
DB 184 AIHDAKNGVLPKPELVDAKGAKWIVLRVDEIKPDPVALLNVGSCOTT 232

RESULT 11  
AAW14246  
ID AAW14246 standard; protein: 233 AA.  
AC AAW14246;  
XX 25-JUN-1997 (first entry)  
DT  
XX Mature pokeweed antiviral protein deletion variant (30-262).  
DE  
XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
XX  
XX Phytoacca americana.  
OS  
XX W09703183-A1.  
PN  
XX 30-JAN-1997.  
PD  
XX 11-JUL-1996; 96WO-US11546.  
PF  
XX 11-JUL-1995; 95US-0500694.  
PR 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PA  
XX Tuner NE;  
PI  
XX WPI: 1997-119040/11.  
DR  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
XX Claim 14: -: 6app; English.  
PS  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SQ Sequence 233 AA;  
Query Match 79.8%; Score 454; DB 18; Length 233;

CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.  
 XX  
 SQ Sequence 229 AA:  
 Query Match 79.8%; Score 454; DB 18; Length 229;  
 Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
 OY 2 GVDSPFKTEAEFLVAIQWSEARFKYIENQKTNFNRAFPDPKVINLEEKWKISE 61  
 11  
 DB 122 GVMSFTEKTEAEFLVAIQWSEARFKYIENQKTNFNRAFPDPKVINLEETWCKIST 180  
 11  
 OY 62 AIHNANAGALPKRLELVDAKGRKVIYLRDEINRDVALLKYVNGTCOTT 110  
 11  
 DB 181 AIHDAKNQVLPKRLLELVDAAGAKWIVLRDEIKPDVALLNYVGGSCOTT 229  
 11  
 RESULT 8  
 AAM14249  
 ID AAM14249 standard; protein; 230 AA.  
 AC AAM14249;  
 XX  
 DT 25-JUN-1997 (first entry)  
 DE Mature pokeweed antiviral protein deletion variant (33-262).  
 XX  
 XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KM bacterium.  
 XX  
 XX PhytoIaccia americana.  
 OS  
 OS  
 PN MO9703183-A1.  
 PD 30-JAN-1997.  
 XX  
 PF 11-JUL-1996; 96WO-US11546.  
 XX  
 PR 11-JUL-1995; 95US-0500694.  
 PR 11-JUL-1995; 95US-0500611.  
 XX  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 PI Turner NE;  
 DR WPI; 1997-119040/11.  
 XX  
 PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 PT and anti-fungal activity in plants and have reduced phytotoxicity  
 XX  
 PS Claim 14: -; 64pp; English.  
 CC Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytotoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.

CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.  
 XX  
 SQ Sequence 230 AA:  
 Query Match 79.8%; Score 454; DB 18; Length 230;  
 Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
 OY 2 GVDSPFKTEAEFLVAIQWSEARFKYIENQKTNFNRAFPDPKVINLEEKWKISE 61  
 11  
 DB 122 GVMSFTEKTEAEFLVAIQWSEARFKYIENQKTNFNRAFPDPKVINLEETWCKIST 181  
 11  
 OY 62 AIHNANAGALPKRLELVDAKGRKVIYLRDEINRDVALLKYVNGTCOTT 110  
 11  
 DB 182 AIHDAKNQVLPKRLLELVDAAGAKWIVLRDEIKPDVALLNYVGGSCOTT 230  
 11  
 RESULT 9  
 AAM14248  
 ID AAM14248 standard; protein; 231 AA.  
 AC AAM14248;  
 XX  
 DT 25-JUN-1997 (first entry)  
 DE Mature pokeweed antiviral protein deletion variant (32-262).  
 XX  
 XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KM bacterium.  
 XX  
 XX PhytoIaccia americana.  
 OS  
 OS  
 PN MO9703183-A1.  
 PD 30-JAN-1997.  
 XX  
 PF 11-JUL-1996; 96WO-US11546.  
 XX  
 PR 11-JUL-1995; 95US-0500694.  
 PR 11-JUL-1995; 95US-0500611.  
 XX  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 PI Turner NE;  
 DR WPI; 1997-119040/11.  
 XX  
 PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 PT and anti-fungal activity in plants and have reduced phytotoxicity  
 XX  
 PS Claim 14: -; 64pp; English.  
 CC Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytotoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

SO Sequence 227 AA:

Query Match 79.8%; Score 454; DB 18; Length 227;  
 Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSPFKTEAFFLLVAIOMSEARFKYENOVKTNFRAPYPPDKVINEBKCKISE 61  
 DB 119 GWSFTEKTEAFFLLVAIOMSEARFKYENOVKTNFRAPYPPDKVINEBKCKISE 178  
 OY 62 AITHNAKNGALPKPPELVDAKGTWIVLRVDEINRDVALLKYNGTCOTT 110  
 DB 179 AITHDAKNGVLPKPELVDAKGTWIVLRVDEINRDVALLKYNGTCOTT 227

RESULT 6  
 AAM14251

ID AAM14251 standard; protein: 228 AA.

AC AAM14251:

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (35-262).

KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KW bacterium.

OS Phytoacca americana.

PN WO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUPF) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14; -: 64pp; English.

CC Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14163-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
 CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation

CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

SO Sequence 228 AA:

Query Match 79.8%; Score 454; DB 18; Length 228;  
 Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSPFKTEAFFLLVAIOMSEARFKYENOVKTNFRAPYPPDKVINEBKCKISE 61  
 DB 120 GWSFTEKTEAFFLLVAIOMSEARFKYENOVKTNFRAPYPPDKVINEBKCKISE 179  
 OY 62 AITHNAKNGALPKPPELVDAKGTWIVLRVDEINRDVALLKYNGTCOTT 110  
 DB 180 AITHDAKNGVLPKPELVDAKGTWIVLRVDEINRDVALLKYNGTCOTT 228

RESULT 7  
 AAM14250

ID AAM14250 standard; protein: 229 AA.

AC AAM14250:

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (34-262).

KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KW bacterium.

OS Phytoacca americana.

PN WO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUPF) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14; -: 64pp; English.

CC Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14163-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
 CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without

CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SQ Sequence 225 AA:  
  
Query Match 79.8%; Score 454; DB 18; Length 225;  
Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
  
OY 2 GVDSEPVKTEAFLLVAIQWSEARFKYIENQVKTNNRPAFPYPPKYINLEKKGKIS 61  
DB 117 GVMSTKTEAFLLVAIQWSEARFKYIENQVKTNNRPAFPYPPKYINLEKKGKIS 176  
OY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCQTT 110  
DB 177 AIHDAKNGVLPKPELVDAKGTWIVLRVDEIKPVDALLNYGSGCQTT 225  
  
RESULT 4  
AAW14253  
ID AAW14253 standard; protein: 226 AA.  
XX  
AC AAW14253;  
XX  
DT 25-JUN-1997 (first entry)  
XX  
DE Mature pokeweed antiviral protein deletion variant (37-262).  
XX  
KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
XX  
OS Phytolacca americana.  
XX  
PN WO9703183-A1.  
XX  
PD 30-JAN-1997.  
XX  
PE 11-JUL-1996; 96WO-US11546.  
XX  
PR 11-JUL-1995; 95US-0500694.  
XX  
PR 11-JUL-1995; 95US-0500611.  
XX  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Turner NE;  
XX  
DR WPI: 1997-119040/11.  
XX  
PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
PS Claim 14: -; 64pp: English.  
XX  
CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal

CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SQ Sequence 226 AA:  
  
Query Match 79.8%; Score 454; DB 18; Length 226;  
Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
  
OY 2 GVDSEPVKTEAFLLVAIQWSEARFKYIENQVKTNNRPAFPYPPKYINLEKKGKIS 61  
DB 118 GVMSTKTEAFLLVAIQWSEARFKYIENQVKTNNRPAFPYPPKYINLEKKGKIS 177  
OY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCQTT 110  
DB 178 AIHDAKNGVLPKPELVDAKGTWIVLRVDEIKPVDALLNYGSGCQTT 226  
  
RESULT 5  
AAW14252  
ID AAW14252 standard; protein: 227 AA.  
XX  
AC AAW14252;  
XX  
DT 25-JUN-1997 (first entry)  
XX  
DE Mature pokeweed antiviral protein deletion variant (36-262).  
XX  
KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
XX  
OS Phytolacca americana.  
XX  
PN WO9703183-A1.  
XX  
PD 30-JAN-1997.  
XX  
PE 11-JUL-1996; 96WO-US11546.  
XX  
PR 11-JUL-1995; 95US-0500694.  
XX  
PR 11-JUL-1995; 95US-0500611.  
XX  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Turner NE;  
XX  
DR WPI: 1997-119040/11.  
XX  
PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
PS Claim 14: -; 64pp: English.  
XX  
CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a

```

XX  New pokeweed antiviral protein (PAP) with similar activity to
PT  ricin - used to treat cancer and as an agricultural chemical
XX
XX  Claim 1; Page 11-13; 14pp: Japanese.
XX
CC  NB: A protein comprising 261 amino acids is claimed.
CC  PAP has a similar activity to ricin, i.e. inhibits protein synthesis.
CC  The protein may be obtained all year round by recombinant DNA
CC  techniques. PAP can be used partic. against cancer and as an
CC  agricultural chemical.
CC  Total mRNA, is extracted from the seeds, leaves and roots of
CC  pokeweed and used to prepare cDNA using PCR. The resultant cDNA is
CC  used to prepare two DNA fractions, which are introduced into a
CC  cloning vector EMBL3 and then into host E.coli PLK-17 (P2) to
CC  produce PAP.
XX
SQ  Sequence 294 AA;
XX
Query Match 80.3%; Score 457; DB 14; Length 294;
Best Local Similarity 82.6%; Pred. No. 7.3e-47;
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
OY 2 GVDSFVKTEAFPLVAIQVSEARFKYIENOVKTNFRAFPDPKVINLEKWKISE 61
DB 177 GVDSFTEKTEAEFLVAIQVSEARFKYIENOVKTNFRAFPNPKVLNLESGWKIST 236
OY 62 AIHNANKGALPKRELVDAGKTKWIVLRVDEINRDVALLKYVNGCOTT 110
DB 237 AIHNANKGALTPLELKNANGSKWIVLRVDIEPDVGLKYVNGCOTAT 285

RESULT 2
AAW14255
ID AAW14255 standard; protein: 224 AA.
AC AAW14255;
XX
XX 25-JUN-1997 (first entry)
XX
DE Mature pokeweed antiviral protein deletion variant (39-262).
XX
KW Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KW translation; broad spectrum; resistance; cell death; sterility; nematode;
KW bacterium.
XX
OS Phytolacca americana.
XX
PN MO9703183-A1.
XX
PD 30-JAN-1997.
XX
PF 11-JUL-1996; 96MO-US11546.
XX
PR 11-JUL-1995; 95US-0500694.
XX 11-JUL-1995; 95US-0500611.
XX
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Turner NE;
XX
DR WPI; 1997-119040/11.
XX
PT New pokeweed antiviral protein mutants - which exhibit anti-viral
PT and anti-fungal activity in plants and have reduced phytotoxicity
XX
XX Claim 14; -: 64pp; English.
XX
CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
CC mutants having reduced phytotoxicity but retaining anti-viral or
CC anti-fungal activity in plants. The sequences' numbering corresponds to
CC anti-fungal activity in plants. The sequences' numbering corresponds to

```

```

CC the 262 amino acid mature protein. The proteins AAW14165-W14217
CC represent serial deletions from the C-terminus whereas sequences
CC AAW14218-55 are serial deletions from the N-terminus. Prior to
CC processing, the protein contains a 22 amino acid N-terminal signal
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a
CC specific adenine residue from a highly conserved stem-loop structure in
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation
CC factor-2 binding thus blocking protein translation. The PAP mutants can
CC confer broad spectrum virus and fungus resistance to plants without
CC causing plant cell death or sterility. They can also confer increased
CC resistance to insects, bacteria and nematodes in plants.
CC N.B. This sequence is not given in the specification but is generated
CC from the wild type sequence reproduced in the specification.
XX
SQ Sequence 224 AA;
XX
Query Match 79.8%; Score 454; DB 18; Length 224;
Best Local Similarity 82.6%; Pred. No. 1.2e-46;
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
OY 2 GVDSFVKTEAFPLVAIQVSEARFKYIENOVKTNFRAFPDPKVINLEKWKISE 61
DB 116 GVDSFTEKTEAEFLVAIQVSEARFKYIENOVKTNFRAFPNPKVLNLESGWKIST 175
OY 62 AIHNANKGALPKRELVDAGKTKWIVLRVDEINRDVALLKYVNGCOTT 110
DB 176 AIHDAKNGVLPKRELVDAGAKWIVLRVDEINRDVALLKYVNGSCOTT 224

RESULT 3
AAW14254
ID AAW14254 standard; protein: 225 AA.
AC AAW14254;
XX
XX 25-JUN-1997 (first entry)
XX
DE Mature pokeweed antiviral protein deletion variant (38-262).
XX
KW Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KW translation; broad spectrum; resistance; cell death; sterility; nematode;
KW bacterium.
XX
OS Phytolacca americana.
XX
PN MO9703183-A1.
XX
PD 30-JAN-1997.
XX
PF 11-JUL-1996; 96MO-US11546.
XX
PR 11-JUL-1995; 95US-0500694.
XX 11-JUL-1995; 95US-0500611.
XX
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Turner NE;
XX
DR WPI; 1997-119040/11.
XX
PT New pokeweed antiviral protein mutants - which exhibit anti-viral
PT and anti-fungal activity in plants and have reduced phytotoxicity
XX
XX Claim 14; -: 64pp; English.
XX
CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
CC mutants having reduced phytotoxicity but retaining anti-viral or
CC anti-fungal activity in plants. The sequences' numbering corresponds to
CC the 262 amino acid mature protein. The proteins AAW14165-W14217
CC represent serial deletions from the C-terminus whereas sequences

```





```

DB      85 -GTVSLGLARVNLVVAFFAVDNRRNVRAVYFRFEINSAELRTVFEVTVANO-----R 137
OY      117 SINNSLYPTMEKKAEV---NSRNOVOLGIQLSSDIGKIS 154
DB      138 PLEYTEDYOSIEKNAKITTGDKSRKRELGLIDLLISTIDKVN 179

RESULT 14
O93Y65 PRELIMINARY: PRT: 294 AA.
ID O93Y65
AC O93Y65;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
OS Dianthus chinensis.
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Caryophyllidae; Magnoliophyta; eudicotyledons; core eudicots;
OC NCBI_TaxID=118431;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20306826; PubMed=10850653;
RA Cho H.J., Lee S.J., Kim S., Kim B.D.;
RT "Isolation and characterization of cDNAs encoding ribosome
RL inactivating protein from Dianthus sinensis L.";
RL Mol. Cells 10:135-141(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF219237; AAK68928.1; -.
DR InterPro: IPR001574; RIP; 1.
DR Pfam: PF00161; RIP; 1.
DR Hydrolyase; Toxin.
KW Hydrolyase; Toxin.
SQ SEQUENCE 294 AA: 33331 MM: 659E72DD847A72D0 CRC64;

Query Match 22.3%, Score 177; DB 10: Length 294;
Best Local Similarity 31.5%, Pred. No. 3.6e-09;
Matches 51; Conservative 30; Mismatches 65; Indels 16; Gaps 6;

OY      2 INTITFDGNGATINKVATFMSLSLNQAKDPKLCYG--IPMLPDTNSTPKYLLVKLOGAN 59
DB      25 VRTITLDIARTAKYSSFLDQIRNNMNDPRLKYCSTEIAVAKPSVADKFLRINFQOPR 84
OY      60 LKTTTLMRLRNLLVMGYSDPFNGNKR-YHIFNDITSTERTDV--ENTLCSSSSSRYAM 116
DB      85 -GTVSLGLARVNLVVAFFAVDNRRNVRAVYFRFEINSAELRTVFEVTVANO-----R 137
OY      117 SINNSLYPTMEKKAEV---NSRNOVOLGIQLSSDIGKIS 154
DB      138 PLEYTEDYOSIEKNAKITTGDKSRKRELGLIDLLISTIDKVN 179

RESULT 15
O93Y64 PRELIMINARY: PRT: 294 AA.
ID O93Y64
AC O93Y64;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
OS Dianthus chinensis.
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Caryophyllidae; Magnoliophyta; eudicotyledons; core eudicots;
OC NCBI_TaxID=118431;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20306826; PubMed=10850653;
RA Cho H.J., Lee S.J., Kim S., Kim B.D.;
RT "Isolation and characterization of cDNAs encoding ribosome
RT inactivating protein from Dianthus sinensis L.";

```

```

RL      Mol. Cells 10:135-141(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF219238; AAK68929.1; -.
DR InterPro: IPR001574; RIP; 1.
DR Pfam: PF00161; RIP; 1.
DR Hydrolyase; Toxin.
KW Hydrolyase; Toxin.
SQ SEQUENCE 294 AA: 33267 MM: E196CE3F1DF97C82 CRC64;

Query Match 22.3%, Score 177; DB 10: Length 294;
Best Local Similarity 31.5%, Pred. No. 3.6e-09;
Matches 51; Conservative 30; Mismatches 65; Indels 16; Gaps 6;

OY      2 INTITFDGNGATINKVATFMSLSLNQAKDPKLCYG--IPMLPDTNSTPKYLLVKLOGAN 59
DB      25 VRTITLDIARTAKYSSFLDQIRNNMNDPRLKYCSTEIAVAKPSVADKFLRINFQOPR 84
OY      60 LKTTTLMRLRNLLVMGYSDPFNGNKR-YHIFNDITSTERTDV--ENTLCSSSSSRYAM 116
DB      85 -GTVSLGLARVNLVVAFFAVDNRRNVRAVYFRFEINSAELRTVFEVTVANO-----R 137
OY      117 SINNSLYPTMEKKAEV---NSRNOVOLGIQLSSDIGKIS 154
DB      138 PLEYTEDYOSIEKNAKITTGDKSRKRELGLIDLLISTIDKVN 179

Search completed: July 2, 2003, 11:42:10
Job time : 23.2767 secs

```

```

Db 26 VTFPLETASKTGCTFLSNLNIIVKDSKLYEGIPMLPAPIKAPAKYLLAELEAKKACTDI 85
Oy 61 KTIITMLRRNNLYWGYSDPFNGNCKRYHIFNDITSTERTVENTLSSSSSRAMSTINY 120
Db 86 -TITLAWSKNDLYVAFTDVOAG-KLRAHFDPDISLATAKAIFPT-----ATGYIOIGY 137
Oy 121 NSLYPTMEKKAENSRNOVOLG 142
Db 138 TSNVYSIEGAAGSN-RVNFOLG 158

RESULT 11
O9M5K6 PRELIMINARY; PRT: 279 AA.
ID O9M5K6
AC O9M5K6
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE RNA-glycosidase (EC 3.2.2.22).
GN CAP30A.
OS Chenopodium album (Lamb's-quarters).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
NCBI_TaxID=3559;
RN
RP SEQUENCE FROM N.A.
RA Park J.S., Cho K.J., Lee S.M., Kim Y.T., Hwang Y.S.;
RT "A cDNA clone encoding a novel ribosome inactivating protein from
RT Chenopodium album L.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL; AF228508; AAF66234.1;
DR HSSP; Q03464; IAPA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP.1.
DR PRINTS; PR00396; SHIGARICIN.
DR HydroLase; Toxin.
SQ SEQUENCE 279 AA; 31377 MW; 2A53300E445DC952 CRC64;

Query Match 24.2%; Score 192; DB 10; Length 279;
Best Local Similarity 36.8%; Pred. No. 1.2e-10;
Matches 53; Conservative 20; Mismatches 63; Indels 8; Gaps 5;

Oy 13 TINKYATFMSLRNOAKDPKLCYGIPLDPDNTSPRYLLVKLOGA--NKTITMLRR 69
Db 37 TONTYNTFMSLRNOAKDPKLCYGIPLDPDNTSPRYLLVKLOGA--NKTITMLRR 96
Oy 70 NNLVWGYSDPFNGNCKRYHIFNDITSTERTVENTLSSSSSRVAMSTINYSLYPTMEK 129
Db 97 NDLVVAAYADKF-GGKVRGHYFKNL-GISTIDEANKVFPNVQDFI--NITYGESYNOIES 152
Oy 130 KAEVNSRNOVOLGIQILSDICKI 153
Db 153 NAGTN-RLSPPLGFDLTKISRNKV 175

RESULT 12
O9AUE3 PRELIMINARY; PRT: 279 AA.
ID O9AUE3
AC O9AUE3
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE RNA-glycosidase (EC 3.2.2.22).
GN CAP30B.
OS Chenopodium album (Lamb's-quarters).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
NCBI_TaxID=3559;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Park J.S., Lee S.M., Kim Y.T., Cho K.J.;
RT "Molecular characterization of a new cDNA clone encoding a ribosome-
RT inactivating protein (CAP30B) from Chenopodium album.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL; AF230812; AAK28323.1;
DR HSSP; Q03464; IAPA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP.1.
DR PRINTS; PR00396; SHIGARICIN.
DR HydroLase; Toxin.
SQ SEQUENCE 279 AA; 31419 MW; 97E934F22C8033AF CRC64;

Query Match 23.7%; Score 188; DB 10; Length 279;
Best Local Similarity 36.6%; Pred. No. 2.9e-10;
Matches 53; Conservative 23; Mismatches 59; Indels 10; Gaps 5;

Oy 13 TINKYATFMSLRNOAKDPKLCYGIPLDPDNTSPRYLLVKLOGA--NKTITMLRR 69
Db 37 TONTYNTFMSLRNOAKDPKLCYGIPLDPDNTSPRYLLVKLOGA--NKTITMLRR 96
Oy 70 NNLVWGYSDPFNGNCKRYHIFNDITSTERTVENTLSSSSSRVAMSTINYSLYPTME 128
Db 97 NDLVVAAYADKF-GGKVRGHYFKNLGIST---IDKAKVFPNVQDFINITYGESYNOIE 151
Oy 129 KAEVNSRNOVOLGIQILSDICKI 153
Db 152 NAGTN-RLSPPLGFDLTKITNKV 175

RESULT 13
O93Y66 PRELIMINARY; PRT: 294 AA.
ID O93Y66
AC O93Y66
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE RNA-glycosidase (EC 3.2.2.22).
GN RiP1.
OS Dianthus chinensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
NCBI_TaxID=118431;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-20306826; PubMed-10850653;
RA Cho H.J., Lee S.J., Kim S., Kim B.D.;
RT "Isolation and characterization of cDNAs encoding ribosome
RT inactivating protein from Dianthus sinensis L.";
RL Mol. cells 10:135-141(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL; AF219236; AAK68927.1;
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP.1.
DR HydroLase; Toxin.
SQ SEQUENCE 294 AA; 33369 MW; 927D93C494EF6C95 CRC64;

Query Match 22.7%; Score 180; DB 10; Length 294;
Best Local Similarity 32.1%; Pred. No. 1.9e-09;
Matches 52; Conservative 29; Mismatches 65; Indels 16; Gaps 6;

Oy 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLDPDNTSPRYLLVKLOGAN 59
Db 25 VTFPLETASKTGCTFLSNLNIIVKDSKLYEGIPMLPAPIKAPAKYLLAELEAKKACTDI 84
Oy 60 KTIITMLRRNNLYWGYSDPFNGNCKRYHIFNDITSTERTVENTLSSSSSRAMSTINY 116

```

```

DR PRINTS:PRO0396: SHIGARICIN.
KW Glycosidase: Hydroxylase: Toxin.
SO SEQUENCE 289 AA; 32652 MW; 132AA966BA27FID CAC64;

Query Match 35.1%; Score 278.5; DB 10; Length 289;
Best Local Similarity 39.3%; Pred. No. 5,3e-19;
Matches 59; Conservative 28; Mismatches 62; Indels 1; Gaps 1;

OY 4 TTTFDAGATATINKATPHESLRNQAKDPKLCYIGPMPLPDINSPFKYLLVQLQANLKT1 63
DB TLVLDDIGGATEKTSDEFTKTRTEKKGADPMYVGLSMPKPKPTPTYLVELKSKDMS1 82
OY 64 TLMTRNNLLYMGASDPFNCKGRHIFNDITSTERTEVENTLSCSSSSRVAMSINYS1 123
DB TLSTLRNLLYVGVSDMYG-KCRHVRPHDSDKKPREQHSLOKADAIIRKPIGVSS 141
OY 124 YPTMEKKAQVSNRNOVOLGIDILSSDGI 153
DB 142 YTEIERKAKVRNKRREIGLVNKLTLPIKV 171

RESULT 10
O39418 PRELIMINARY; PRT. 272 AA.
AC O39418:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Antiviral protein precursor (Ribosome-inactivating protein) (RRNA N-
DE glycosidase) (Polynucleotide:adenosine glycosidase) (EC 3.2.2.22)
DE (BETAVULGIN) (BVG).
GN RIP OR BETAVULGIN OR BVG.
OS Beta vulgaris (Sugar beet).
OC Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.
CC NCBI_taxonomy:3555;
RN [1]
RX SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=SEEDLING;
RX MEDLINE=96235141; PubMed=8666251;
RA Horning E., Wajant H., Jeske H., Mundry K.-W.;
RT "Cloning of a cDNA encoding a new ribosome-inactivating protein from
RT Beta vulgaris vulgaris (mangold).";
RL Gene 170:233-236(1996).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
CC SYNTHESIS IN VITRO. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR
CC SUICIDE UPON INVASION BY A VIRUS.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
CC PROTEINS.
CC -1- SIMILARITY: BELONGS TO TYPE 1 RIP.
DR EMBL: X85967; CAAS9952.1; .
DR HSSP: 003464; JAP.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PRO0396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; FALSE_NEG.
KW Hydroxylase: Glycosidase: Antiviral; Protein synthesis inhibitor; Toxin;
KW Multigene family; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 272 ANTIVIRAL PROTEIN.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 272 AA; 30168 MW; 77DD0917FD12FDFP CRC64;

Query Match 24.3%; Score 192.5; DB 10; Length 272;
Best Local Similarity 38.7%; Pred. No. 1e-10;
Matches 55; Conservative 20; Mismatches 54; Indels 13; Gaps 5;

OY 5 ITFDAGNATINKYATFMEESLRNOAKDPKLCYIGPMPLPDINSPFKYLLVQLQANLKT1 60

```

```

Db      121 SRPPTLESKAGVRSQVOLGIQILDSNIGKIS 153
      1 |||:| |||:||||||| |||:|
RESULT 5
ID 0941G8 PRELIMINARY: PRT: 313 AA.
AC 0941G8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
GN PAP.
OS Phytolacca aclinosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=107615;
RN [1]
RP SEQUENCE FROM N.A.
RA Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AY049785; AAL15442.1;
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
KW Hydrolase; Toxin.
SQ SEQUENCE 313 AA: 35059 MW: E478CD571C17885 CRC64:

Query Match      75.0%; Score 595; DB 10; Length 313;
Best Local Similarity 71.9%; Pred. No. 1,3e-49;
Matches 110; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFMESLRNOAKDKPKLKCVCIGPMLPDTNSTPKYLLVLOGANLK 61
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 23 VNTIIVNGSTIISKATFLDNRNKAQPSLKCVCIGPMLPNTNPKYLVVLEQSNKK 82
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
QY 62 TTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 83 TTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCPNRSRVKININD 142
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
QY 122 SLPTMEKKAEVNSRNQVOLGIQILSSDIGKIS 154
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 143 SRPPTLESKAGVRSQVOLGIQILDSNIGKIS 175
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|

RESULT 6
ID 09XFF8 PRELIMINARY: PRT: 315 AA.
AC 09XFF8:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
GN PIP2.
OS Phytolacca insularis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=63744;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:20505377; PubMed:11052196;
RA Song S.K., Choi Y., Moon Y.H., Kim S.C., Choi Y.D., Lee J.S.;
RT "Systemic induction of a Phytolacca insularis antiviral protein gene
RT by mechanical wounding, jasmonic acid, and abscisic acid.";
RL Plant Mol. Biol. 43:439-450(2000).
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF141331; AAD32679.1;

```

```

DR HSP: O03464; JAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; UNKNOWN_1.
KW Hydrolase; Toxin.
SQ SEQUENCE 315 AA: 35728 MW: F85DE21154B5FA15 CRC64:

Query Match      68.4%; Score 542.5; DB 10; Length 315;
Best Local Similarity 71.1%; Pred. No. 1,6e-44;
Matches 108; Conservative 21; Mismatches 20; Indels 3; Gaps 3;

QY 3 INTTFDAGNATINKYATFMESLRNOAKDKPKLKCVCIGPMLPDTNSTPKYLLVLOGANLK 62
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 28 NPTTFEAGNATINKYATFMESLRNOAKDKPKLKCVCIGPMLPDTNSTPKYLLVLOGANLK 87
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
QY 63 TTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 88 TTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCPNRSRVKININD 146
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
QY 122 SLPTMEKKAEVNSRNQVOLGIQILSSDIGKIS 153
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 147 SSYPALKKRVG-RSRKQVOLGIQILSSDIGKIS 177
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|

RESULT 7
ID 08RYA4 PRELIMINARY: PRT: 339 AA.
AC 08RYA4:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ribosome inactivating protein type I precursor.
OS Phytolacca americana (Common pokeweed) (Virginia pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Park S.-W., Lawrence C.B., Linden J.C., Vivanco J.M.;
RT "Characterization of a novel ethylene-inducible rice-american-
RT protein exuded from root cultures of Phytolacca americana."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY071928; AAL61546.1;
KW Signal.
FT SIGNAL.
SQ SEQUENCE 339 AA: 37978 MW: 7D47BDC2DED965F CRC64:

Query Match      66.5%; Score 527; DB 10; Length 339;
Best Local Similarity 66.9%; Pred. No. 5,4e-43;
Matches 103; Conservative 18; Mismatches 29; Indels 4; Gaps 1;

QY 5 INTTFDAGNATINKYATFMESLRNOAKDKPKLKCVCIGPMLPDTNSTPKYLLVLOGANLK 60
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 49 ISFDVGSATISKTTFOESLRNOAKDKPKLKCVCIGPMLPDTNSTPKYLLVLOGANLK 108
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
QY 61 TTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 120
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 109 TTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCPNRSRVKININD 168
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
QY 121 NSLPTMEKKAEVNSRNQVOLGIQILSSDIGKIS 154
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|
DB 169 DSRYPTEKKAEGVSGVOLGIETILNSIGKIS 202
   |||:| |||:||||||| |||:| |||:||||||| |||:| |||:||||||| |||:|

RESULT 8
ID P93077 PRELIMINARY: PRT: 302 AA.
AC P93077:
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

```

QY 2 INITTPGAGAAITNKATATEMESLRNOKPDKCYGIPMLPTNSTPKYLLVXLOGANLK 61

Db 25 INITTPDAGAAITNKATATEMESLRNOKPDKCYGIPMLPTNSTPKYLLVXLOGANLK 84

QY 62 TITLMLRRNNLYMGSDPFGNKKCRHYHENDITSTERTDVENTLSSSSSRVAMSTIYN 122

Db 85 TITLMLRRNNLYMGSDPFGNKKCRHYHENDITSTERTDVENTLSSSSSRVAMSTIYN 144

QY 122 SLPTMEKKAENVSRNOVLOGIQLISSDICKITS 154

Db 145 SLPTMEKKAENVSRNOVLOGIQLISSDICKITS 177

RESULT	2
08S946	
ID	08S946
AC	08S946;
DT	01-JUN-2002 (TREMBLrel. 21, Created)
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	PAP-S2 (Fragment).
GN	PAP52.
OS	Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX	NCBI_TaxID=3527;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Honjo E., Watanabe K.;
RT	"Cloning of genomic DNA encoding two types of pokeweed antiviral
RT	protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT	their recombinant proteins with other PAP isoforms.";
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB071855; BAB6350.1; -.
FT	NON_TER
FT	1 262
FT	1 262
SO	SEQUENCE 262 AA; 29486 MW; AE2D010A73C9D18B CRC64;

Query Match	97.5%	Score 773	DB 10	Length 265
Best Local Similarity	97.4%	Pred. No. 6e-67		
Matches 149	Conservative 3	Mismatches 1	Indels 0	Gaps 0
QY	2	INTFTDAGNATINKYATFMEESLRNQAQDKPLKCYGIPMLPDYNTSTPKYLYLVQAGANLK	61	
Db	1	INTFTFDAGNSTINKYATFMEESLRNQAQDKPLKCYGIPMLPDYNTSTPKYLYLVQAGANLK	60	
QY	62	TTTTLRLRRNNLYVMKYSDFPFGNKCRCRHHFNDITSTERDVENTLCCSSSSRYAMSINYN	121	
Db	61	TTTTLRLRRNNLYVMKYSDFPFGNKCRCRHHFNDITSTERDVENTLCCSSSSRYAMSINYN	120	
QY	122	SLYPTMEKKAEYNSRQVQGLQTLSSDICKIS	154	
Db	121	SLYPTLEKKAELYNSRQVQGLQTLSSDICKIS	153	

RESULT 3		
ID	08S947	PRELIMINARY;
AC	08S947:	PRT; 261 AA.
DT	01-JUN-2002 (TREMBLrel, 21, Created)	
DT	01-JUN-2002 (TREMBLrel, 21, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel, 21, Last annotation update)	
DE	PAP-S1 (Fragment).	
DE	PAP-S1	
OS	Physalacca americana (Common pokeweed) (Virginiaan pokeweed).	
OS	Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta;	
OC	Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots:	
OC	Caryophyllales; Caryophyllaceae; Physalacca.	
OX	NCBI_TaxID=3527;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

RA Honjo E. Watanabe K.;  
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral  
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of  
RT their recombinant proteins with other PAP isoforms";  
RL submitted (SEPT-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AB071854; BAB86349.1; --  
FT NON\_TER 261 1  
FT NON\_TER 261 1  
SO SEQUENCE 261 AA: 29199 MW: D88B998BEFE1F989 CRC64;

Query Match	84.68;	Score 670.5;	DB 10;	Length 261;
Best Local Similarity	86.38;	Pred. No. 5.1e-57;		
Matches 132;	Conservative 8;	Mismatches 12;	Indels 1;	Gaps 1

QY 2 INTITFEDACNATINKATFAMESLRNQADPKCKGCIPLDPTNSTPKYLLLVKIQGANLK 61

Db 1 INTITFDACNATINKATFAMESLRNEADPSLCKGCIPLDPTNSTIKYLLLVKIQGASLK 60

QY 62 TITLMLRRNNLVVMGSDPFGNCKRHAIFENDITSTERTDVENTLCSSSSPRVMASTNYN 121

Db 61 TITLMLRRNNLVVMGSDPYD-NKCRTHIFENDIKTEYSDEVNTLCPSNBRVAKPINYN 119

QY 122 SLYPTMEKRAEYNSRNOVQGIQLISSDIGKIS 154

Db 120 GLYPTLEKRAGYTSRNQVQGIQLISSDIGKIS 152

RESULT 4		
ID	Q9ATB3	PRT: 237 AA.
AC	Q9ATB3;	PRELIMINARY;
DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	RNA-glycosidase (EC 3.2.2.22) (Fragment).	
GN	MPAP.	
OS	Phytolacca americana (Common pokeweed) (Virginian pokeweed).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
OC	Caryophyllidae; Caryophyllales; Phytolacaceae; Phytolacca.	
OX	NCBI_TaxId=3527;	

RP	SEQUENCE FROM N.A.
RA	Chen D., Mang X., Zhou G.: "Pokeweed antiviral protein gene, partial cds."
RT	Submitted (JAN-2001) to the EMBL/Genbank/DDJB databases.
RL	-:- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.
CC	-:- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
CC	EMBL: AF38910; AAK21951.1; -:-
DR	HSSP: P10297; IQCG.
DR	InterPro: IPR001574; RIP.
DR	Pfam: PF00161; RIP_1.
DR	PRINTS: PR00396; SHIGARICIN.
DR	PROSITE: PS00275; SHIGA_RICIN; 1.
KW	Hydrolase; Toxin;
FT	NON_TER 1
FT	NON_TER 237
SO	SEQUENCE 237 AA; 26534 MW; FE4ADCEED30464783 CRC64;

[illegible]

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 22.2767 Seconds

(without alignments)  
1424.413 Million cells updates/sec

Title: US-09-978-274A-6

Perfect score: 793  
Sequence: 1 MINTTFDAGNATINKATF.....SRNOVQLGILSSDICKIS 154

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mnc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.fodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	788	99.4	314	10	P93444
2	773	97.5	262	10	O8S946
3	670.5	84.6	261	10	O8S947
4	598	75.4	237	10	O9ATB3
5	595	75.0	313	10	O941G8
6	542.5	68.4	313	10	O9XFF8
7	527	66.5	339	10	O8RYA4
8	399	50.3	302	10	P93077
9	278.5	35.1	289	10	P93261
10	192.5	24.3	272	10	O39418
11	192	24.2	279	10	O9MSK6
12	188	23.7	279	10	O9AUE3
13	180	22.7	294	10	O93Y66
14	177	22.3	294	10	O93Y65
15	177	22.3	294	10	O93Y64
16	152	19.2	319	10	O8VWY2

17	129.5	16.3	573	10	O8W2E8	O8W2E8 iris hollan
18	128.5	16.2	279	10	O92T25	O92T25 amarantus
19	125	15.8	300	10	O04356	O04356 iris hollan
20	124.5	15.7	251	10	O48859	O48859 amarantus
21	124	15.6	305	10	O8W4U4	O8W4U4 bougainvill
22	123	15.5	300	10	O04357	O04357 iris hollan
23	119	15.0	258	10	O9S9E4	O9S9E4 gelonium mu
24	116	14.6	564	10	O9AVR2	O9AVR2 sambucus eb
25	115.5	14.6	592	10	O8W2E7	O8W2E7 iris hollan
26	115	14.5	278	10	O00980	O00980 luffa cylin
27	115	14.5	563	10	O945S2	O945S2 sambucus ni
28	113	14.2	547	10	O9M6E9	O9M6E9 abrus prec
29	112.5	14.2	103	10	O05148	O05148 seponaria o
30	112.5	14.2	566	10	O04072	O04072 sambucus ni
31	112	14.1	298	10	O04358	O04358 iris hollan
32	112	14.1	541	10	O41174	O41174 ricinus com
33	111.5	14.1	247	10	O9LRE3	O9LRE3 trichosan
34	111.5	14.1	289	10	O94KE4	O94KE4 trichosan
35	110.5	13.9	270	10	O41611	O41611 trichosan
36	110.5	13.9	604	10	O9M654	O9M654 polygonat
37	108	13.6	251	10	O96235	O96235 abrus prec
38	108	13.6	251	10	O96236	O96236 abrus prec
39	108	13.6	251	10	O96237	O96237 abrus prec
40	108	13.6	252	10	O38761	O38761 abrus prec
41	106.5	13.4	580	10	O94BW3	O94BW3 cinnaomum
42	105.5	13.3	289	10	O41216	O41216 trichosan
43	105	13.2	563	10	O04367	O04367 sambucus ni
44	104.5	13.2	581	10	O94BW5	O94BW5 cinnaomum
45	103.5	13.1	580	10	O94BW4	O94BW4 cinnaomum

## ALIGNMENTS

RESULT 1  
P93444 PRELIMINARY: PRT: 314 AA.  
ID P93444  
AC P93444  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE RNA - glycosidase precursor (EC 3.2.2.22).  
OS PAP-S.  
GN Phytolacca americana (Common pokeberry) (Virginian pokeweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SEED;  
RX MEDLINE=97263479; PubMed=9109394;  
RA Poyet J.L., Hoeveler A.;  
RT "cDNA cloning of the gene encoding the Antiviral Protein from the  
RT seeds of Phytolacca americana and its expression in E.coli.";  
RL FEBS Lett. 406:97-100(1997).  
CC -1- CATALYTIC ACTIVITY: ENDOTHEROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
EMBL: X98079; CA66702.1; -;  
DR HSSP; Q03464; IAPA.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Hydrolyase; Signal; Toxin.  
FT SIGNAL  
FT CHAIN 1 24  
FT POTENTIAL.  
SQ SEQUENCE 314 AA; 35323 MW; A89E3CE5789F9E CRC64;  
Query Match 99.4%; Score 788; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 2.6e-68;  
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Search completed: July 2, 2003, 11:37:39
Job time : 7.05346 secs
```





```

SQ NON_TER      32      32      45BAFEBEE2473CE7 CRC64;
FD SEQUENCE     32 AA: 3491 MW: 48000
Query Match          16.5% Score 131; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 6.2e-07;
Matches 24; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy      2 INTTFPDAGNATINKYATFMESLNRQAKDRL 33
Db      1 VSTTFPDGSAITISKYTTFLESLNRQAKDPSL 32
:::||||| :|||:| |:|||:||||| |||
RESULT 12
R1P1_TRIAN STANDARD: PRT: 294 AA.
AC P56626; Q9ZOX7;
DT 15-DEC-1998 (Rel. 37, Created)
DR 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type I ribosome-inactivating protein trichosanguina precursor (rRNA
   N-glycosidase) (EC 3.2.2.22) (RIP) (Trichoanguin).
GN TCA.
OS Trichosanthes angulina (Snake gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=50544;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=cv. Angulina; TISSUE=seed;
RX MEDLINE=99132006; PubMed=9931318;
RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,
   Lin J.-Y.;
RT "Purification, characterization and molecular cloning of trichoangulin,
   a novel type I ribosome-inactivating protein from the seeds of
   Trichosanthes angulina.";
RL Biochem. J. 338:211-219(1999).
RN [2]
RP SEQUENCE OF 20-264.
RC TISSUE=seed;
RA Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;
RT "Amino acid sequence of trichoangulina, a ribosomal-inactivating
   protein from Trichosanthes angulina seeds.";
RL J. Biomed. Sci. 5:178-186(1996).
CC - FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN
   RIBOSOMES.
CC - CATALYTIC ACTIVITY: Endohydrolasis of the N-glycosidic bond at one
   specific adenosine on the 28S rRNA.
CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isdb-sib.ch/announce/
   or send an email to license@sib-sib.ch).
CC -----
EMBL: AF055086; AAD02686.1; -
DR HSSP: P33185; 1BRV.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PS00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; FALSE_NEG.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
   Glycoprotein; Signal.
FT SIGNAL 1..19
FT CHAIN 20..264
FT PROPEP 265..294
FT ACT_SITE 177..180
FT ACT_SITE 180..180
FT BY SIMILARITY.
FT BY SIMILARITY.

```

```

50  QUERY MATCH          16.5%  SCORE 130.5  DB 1  LENGTH 294  ;
51  BEST LOCAL SIMILARITY 27.2%  PRED. NO. 1.1e-05;
52  MATCHES 41;  CONSERVATIVE 30;  MISMATCHES 63;  INDELS 17;  GAPS 6;
53
54  FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (PROBABLE).
55  FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (PROBABLE).
56  FT CONFLICT 51 51 C -> Y (IN REF. 2).
57  FT CONFLICT 65 65 W -> R (IN REF. 2).
58  FT CONFLICT 84 84 N -> D (IN REF. 2).
59  FT CONFLICT 152 152 A -> S (IN REF. 2).
60  FT CONFLICT 174 174 C -> S (IN REF. 2).
61  FT CONFLICT 245 245 N -> H (IN REF. 2).
62  FT SEQUENCE 294 AA; 32234 MW; DA4FB87CE3290994 CXC64;
63
64  Query Match          16.5%  SCORE 130.5  DB 1  LENGTH 294  ;
65  BEST LOCAL SIMILARITY 27.2%  PRED. NO. 1.1e-05;
66  MATCHES 41;  CONSERVATIVE 30;  MISMATCHES 63;  INDELS 17;  GAPS 6;
67
68  2 INTTFDAGNATINKYATFMESLRNQAOKPKLCYGIPLMDPNTSPKYL-LVKLOGANL 60
69  18 IGDVSFDSTATKKSYSFFITQLRDLALPTQGTVC-GIFLLPSTASGSQMFPPFLNTYND 76
70  KTIITLMLRRNLVYWG-Y-SDFPNKKCKYHIFNDITSERFDVENTLSSSSSRVAMSIN 119
71  ETIVVAVNTVNTVYVAIRDAVS-----YFED--TPAEAFKLIFAGTIVKLPYSGN 127
72
73  120 YNSLYPTMKRAEVNSRNQVOLIQLITSSDI 150
74  128 YDKLQSVYKQ-----RDMIELGLIPALSSAI 153
75
76  RESULT 13
77  RIP3_SAPOF
78  ID RIP3_SAPOF STANDARD: PRT: 236 AA.
79  AC P27560.
80  DT 01-AUG-1992 (Rel. 23, Created)
81  DT 01-AUG-1992 (Rel. 23, Last sequence update)
82  DT 15-JUN-2002 (Rel. 41, Last annotation update)
83  DE Ribosome-inactivating protein saporin-3 (SAP-3) (SO-3) (rRNA N-
84  glycosidase) (EC 3.2.2.22) (Fragment).
85  SAFP.
86  GN Saporaria officinalis (Common soapwort).
87  OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
88  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
89  CC Caryophyllales; Caryophyllaceae; Saponaria.
90  OX NCBI_TaxID=3572;
91  RN
92  RP SEQUENCE FROM N.A.
93  RX MEDLINE=92049247; PubMed=1719367;
94  RA Forcham-Skelton A.P., Taylor P.E., Hartley M.R., Croy R.B.D.;
95  RT "Characterisation of saporin genes: in vitro expression and ribosome
96  inactivation.";
97  RL Mol. Genet. 229:460-466(1991).
98  CC -I- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
99  CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR
100 CC PHARMACOLOGICAL APPLICATIONS.
101 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
102 CC specific adenosine on the 28S rRNA.
103 CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
104 CC TYPE 1 RIP SUBFAMILY.
105 CC
106 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
107 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
108 CC the European Bioinformatics Institute. There are no restrictions on its
109 CC use by non-profit institutions as long as its content is in no way
110 CC modified and this statement is not removed. Usage by and for commercial
111 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/sib.ch).
112 CC or send an email to license@sib-sib.ch).
113 CC
114 DR EMBL, X59326; CAA1949.1; -
115 DR PIR, S17932; S17932.
116 DR HSSP, P10297; I0CG.
117 DR InterPro: IPR001574; RIP.
118 DR Pfam: PF00161; RIP; 1.
119 DR PROSITE: PS00275; SHIGA-RICIN; 1.
120 KM Plant defense. Protein synthesis inhibitor; Hydrolase; Toxin;
121 KM Multigene family.

```



```

CC EMBL: X69134; CAA4888.1;
DR HSSP: P10297; 10CG.
DR Interpro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
KW Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;
KM Multigene family.
FT ACT_SITE 176
SQ SEQUENCE 253 AA; 28553 MW; 161319102AB20539 CRC64;

Query Match 23.3%; Score 184.5; DB 1; Length 253;
Best Local Similarity 30.8%; Pred. No. 4,3e-11;
Matches 49; Conservative 37; Mismatches 62; Indels 11; Gaps 5;

OY 2 INTITFDAGNATINVTAFMESLRNQAQDKPKCYGIPM-LPDTNSTPKYLKLGANL 60
DB 1 VTSITLDLVNPTAGGYSSVFDKIRNNVDPNKKYGTDAVIGPPSKKEFLINQSSR- 59
OY 61 KTTITMLRRNNLYVWGYSDFPFGNKCR-YHIFNDITSPERTDVENTLCSSSSRVAMSIN 119
DB 60 GTVSLGLKRDNLVVAIVYALMDNTNVRAYFRSEITSAELT---ALPEATTANQKALE 115
OY 120 YNSLYPTMEKAEV---NSRNQVQIGIQLSSDGKIS 154
DB 116 YTEDYQSIEKKNQITQGSKRELGLDILLTSMQAVN 154

RESULT 8
RIP2_SAPOR
ID RIP2_SAPOR STANDARD: PRT: 292 AA.
AC P27559; Q9SAP5; Q41390;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-2 precursor (SAP-2) (SO-2)
DE (rRNA N-glycosidase) (EC 3.2.2.22).
GN SAP2.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92049247; PubMed=1719367;
RA Fordham-Skelton A.P., Taylor P.E., Hartley M.R., Croy R.R.D.;
RT "Characterisation of saporin genes: In vitro expression and ribosome
RT inactivation."
RL Mol. Gen. Genet. 229:460-466(1991).
RN [2]
RP SEQUENCE OF 25-284 FROM N.A.
RC TISSUE=Leaf.
RX MEDLINE=93203250; PubMed=8454624;
RA Bartelme I., Martineau D., Ong M., Matsunami R., Ling N.,
RA Benatti L., Cavallaro U., Sorla M., Lappi D.A.;
RT "The expression of saporin, a ribosome-inactivating protein from the
RT plant Saponaria officinalis, in Escherichia coli."
RL J. Biol. Chem. 268:6541-6548(1993).
CC -I- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR
CC PHARMACOLOGICAL APPLICATIONS.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/)

```

```

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X59255; CAA41948.1;
DR DR EMBL: X69132; CAA48886.1;
DR DR EMBL: X69133; CAA48887.1;
DR PIR: S17933; RLONG2.
DR HSSP: P10297; 10CG.
DR Interpro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
KW Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KM Multigene family.
FT SIGNAL 1
FT CHAIN 25 292 RIBOSOME-INACTIVATING PROTEIN SAPORIN-2.
FT ACT_SITE 200 200 BY SIMILARITY.
FT VARIANT 72 72 D->E.
SQ SEQUENCE 292 AA; 32810 MW; FA143CE1BE88976 CRC64;

Query Match 23.1%; Score 183.5; DB 1; Length 292;
Best Local Similarity 32.5%; Pred. No. 6,4e-11;
Matches 49; Conservative 33; Mismatches 58; Indels 11; Gaps 5;

OY 2 INTITFDAGNATINVTAFMESLRNQAQDKPKCYGIPM-LPDTNSTPKYLKLGANL 60
DB 25 VTSITLDLVNPTAGGYSSVFDKIRNNVDPNKKYGTDAVIGPPSKKEFLINQSSR- 83
OY 61 KTTITMLRRNNLYVWGYSDFPFGNKCR-YHIFNDITSPERTDVENTLCSSSSRVAMSIN 119
DB 84 GTVSLGLKRDNLVVAIVYALMDNTNVRAYFRSEITSAELT---ALPEATTANQKALE 139
OY 120 YNSLYPTMEKAEV---NSRNQVQIGIQL 146
DB 140 YTEDYQSIEKKNQITQGSKRELGLDILL 170

RESULT 9
RIP0_DIACA
ID RIP0_DIACA STANDARD: PRT: 293 AA.
AC P24476;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein DAP-30 precursor (Ribosome-inactivating protein)
DE (rRNA N-glycosidase) (EC 3.2.2.22) (Dianthin 30).
OS Dianthus caryophyllus (Carnation) (Clove pink).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
OX NCBI_TaxID=3570;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91355219; PubMed=1840496;
RA Legname G., Bellista P., Gromo G., Modena D., Keen J.N., Roberts L.M.,
RA Lord J.M.;
RT "Nucleotide sequence of cDNA coding for dianthin 30, a ribosome
RT inactivating protein from Dianthus caryophyllus."
RL Biochim. Biophys. Acta 1090:119-122(1991).
RN [2]
RP SEQUENCE OF 24-82.
RC TISSUE=Leaf.
RX MEDLINE=92037998; PubMed=1936243;
RA Lee-Huang S., Kung H.-F., Huang P.L., Huang P.L., Li B.-Q., Huang P.,
RA Huang H.I., Chen H.-C.;
RT "A new class of anti-HIV agents: GAP31, DAPs 30 and 32."
RL FEBS Lett. 291:139-144(1991).
CC -I- FUNCTION: SINGLE-CHAIN RIBOSOME-INACTIVATING PROTEIN, POSSESSING
CC HIGH ANTIVIRAL POTENCY AND LOW TOXICITY TO NORMAL CELLS IN CULTURE
CC AND TO INACT ANIMALS. CAPABLE OF INHIBITING HIV-1 INFECTION AND
CC REPLICATION.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

```

DR EMBL: X15655; CAA33685.1; -  
DR EMBL: S57638; AAB25863.1; -  
DR EMBL: X69135; CAA48889.1; -  
DR EMBL: X64917; CAA46110.1; -  
DR EMBL: A00352; CAA00055.1; -  
DR PIR: S05205; S05205.  
DR HSSP: P10297; 10CG.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PRINTS: PR00396; SHIGA.RICIN.  
DR PROSITE: PS00275; SHIGA.RICIN. 1.  
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; signal;  
KM Multigene family.  
FT SIGNAL 1 24  
FT CHAIN 25 277 RIBOSOME-INACTIVATING PROTEIN SAPORIN-6.  
FT PROPEP 278 299 POTENTIAL.  
FT ACT\_SITE 200 200 BY SIMILARITY.  
FT CARBOHD 283 283 N-LINKED (GLUCNA. . .) (POTENTIAL).  
FT VARIANT 72 72 E -> D.  
FT VARIANT 115 115 R -> K.  
FT CONFLICT 123 123 S -> L (IN REF. 2 AND 4).  
FT CONFLICT 212 212 I -> T (IN REF. 1; AA SEQUENCE).  
SQ SEQUENCE 299 AA: 33607 MW: 480312958BAE79B CRC64:

Query Match 24.1%; Score 191.5; DB 1; Length 299;  
Best Local Similarity 31.4%; Pred. No. 1, 1e-11;  
Matches 50; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

OY 2 INTTFDAGNATINKYATFMESLRQAKDPKLCYGPV-LPDNTSPKYLVLKQANL 60  
DB 25 VTSITLDLVNPTAGQSSFDVKIRNNVMDPKLKGCTGTDIAVIGPSKKEFLRINFQSR- 83  
OY 61 KTIILMLRRNLVWYGSDPENGKCR-YHIFNDITSTERPDVENTLSSSSSRVAMSIN 119  
DB 84 GTVSLGKRDMLVYVAYLAMDNVNNRAYFRSEITSAEST-ALFPEATYANQKALE 139  
OY 120 YNSLYPTMEKRAEV-----NSRNOVLGIQLSSDIGKS 154  
DB 140 YTEDYQSTLEKNAQITQGDGSRKEGLGIDLLTSMKAVN 178

RESULT 6  
RIP5\_SAPORIN STANDARD: PRT: 253 AA.  
AC 041389:

DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein saporin-5 (EC 3.2.2.22) (SAP-5) (rRNA N-glycosidase).  
GN SAP5.

OS Saponaria officinalis (Common soapwort).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Caryophyllaceae; Saponaria.  
OX NCBI\_TaxID=3572;

RN SEQUENCE FROM N.A.

RP TISSUE-Leaf;

RC MEDLINE=93203250; PubMed=8454624;

RA Barthelmy I., Martineau D., Ong M., Matsunami R., Ling N.,

Benatti L., Cavallaro U., Soria M., Lappi D.A.;

"The expression of saporin, a ribosome-inactivating protein from the

plant *Saponaria officinalis*, in *Escherichia coli*."

J. Biol. Chem. 268:6541-6548(1993).

CC FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS

CC CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one

CC specific adenosine on the 28S rRNA.

CC SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 1 RIP SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X69131; CAA48885.1; -  
DR EMBL: X69132; CAA48886.1; -  
DR HSSP: P10297; 10CG.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PROSITE: PS00275; SHIGA.RICIN. 1.  
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;  
KM Multigene family.  
FT ACT\_SITE 176 176 BY SIMILARITY.  
SQ SEQUENCE 253 AA: 28556 MW: 539693E13D0F594D CRC64:

Query Match 23.3%; Score 184.5; DB 1; Length 253;  
Best Local Similarity 30.8%; Pred. No. 4, 3e-11;  
Matches 49; Conservative 37; Mismatches 62; Indels 11; Gaps 5;

OY 2 INTTFDAGNATINKYATFMESLRQAKDPKLCYGPV-LPDNTSPKYLVLKQANL 60  
DB 1 VTSITLDLVNPTAGQSSFDVKIRNNVMDPKLKGCTGTDIAVIGPSKKEFLRINFQSR- 59  
OY 61 KTIILMLRRNLVWYGSDPENGKCR-YHIFNDITSTERPDVENTLSSSSSRVAMSIN 119  
DB 60 GTVSLGKRDMLVYVAYLAMDNVNNRAYFRSEITSAEST-ALFPEATYANQKALE 115  
OY 120 YNSLYPTMEKRAEV-----NSRNOVLGIQLSSDIGKS 154  
DB 116 YTEDYQSTLEKNAQITQGDGSRKEGLGIDLLTSMKAVN 154

RESULT 7  
RIP7\_SAPORIN STANDARD: PRT: 253 AA.  
AC 041391:

DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein saporin-7 (SAP-7) (rRNA N-glycosidase) (EC 3.2.2.22).  
GN SAP7.

OS Saponaria officinalis (Common soapwort).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Caryophyllaceae; Saponaria.  
OX NCBI\_TaxID=3572;

RN SEQUENCE FROM N.A.

RP TISSUE-Leaf;

RC MEDLINE=93203250; PubMed=8454624;

RA Barthelmy I., Martineau D., Ong M., Matsunami R., Ling N.,

Benatti L., Cavallaro U., Soria M., Lappi D.A.;

"The expression of saporin, a ribosome-inactivating protein from the

plant *Saponaria officinalis*, in *Escherichia coli*."

J. Biol. Chem. 268:6541-6548(1993).

CC FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS

CC CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one

CC specific adenosine on the 28S rRNA.

CC SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 1 RIP SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Antiviral protein 2 precursor (PAP-II) (Ribosome-inactivating protein)  
 DE (tRNA N-glycosidase) (EC 3.2.2.22).  
 GN PAP2 OR PAP11.  
 OS Phytolacca americana (Common pokeweed) (Virginia pokeweed).  
 OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.  
 OC NCBI\_TaxID=3527;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Leaf;  
 RX MEDLINE=94307398; PubMed=8034016;  
 RA Poyet J.-L., Radom J., Hoeveler A.;  
 RT "Isolation and characterization of a cDNA clone encoding the pokeweed  
 RT antiviral protein II from Phytolacca americana and its expression in  
 RT E. coli.";  
 RL FEBS Lett. 347:268-272(1994).  
 RN [2]  
 RP SEQUENCE OF 26-55.  
 RC TISSUE-Leaf;  
 RX MEDLINE=85023392; PubMed=6091760;  
 RA Bjorn M.J., Larrick J., Platak M., Wilson K.J.;  
 RT "Characterization of translational inhibitors from Phytolacca  
 RT americana. Amino-terminal sequence determination and antibody-  
 RT inhibitor conjugates.";  
 RL Biochim. Biophys. Acta 790:154-163(1984).  
 CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS. INHIBITS PROTEIN  
 CC SYNTHESIS IN BOTH PROKARYOTES AND EUKARYOTES.  
 CC -1- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LATE SUMMER LEAVES.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED PROGRESSIVELY WITH THE AGING OF THE  
 CC PLANT.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: X78628; CAA5342.1; -;  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP: 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGARICIN: 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KM Toxin; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 ? ANTIVIRAL PROTEIN 2.  
 FT PROPEP 2 310  
 FT ACT\_SITE 197 197 BY SIMILARITY.  
 FT DISULFD 57 284 BY SIMILARITY.  
 FT DISULFD 106 123 BY SIMILARITY.  
 SO SEQUENCE 310 AA; 34694 MW; 4D3BB001D7259D9F CRC64;  
 Query Match 32.9%; Score 261; DB 1; Length 310;  
 Best Local Similarity 41.2%; Pred. No. 1.5e-18;  
 Matches 63; Conservative 20; Mismatches 60; Indels 10; Gaps 5;  
 OY 3 NTTFDAGNATINKYATFMESLRNQAQDKPKLKYGIPLPTNSTPKYLLVKGLOGANKT 62  
 DB 25 SNIVDEVNATPETSNSLTSREAVXKDKLTHCHMIMATLTTEQPKVVLVDLKRGS-GT 83  
 OY 63 ITLMIRNNLVYMGSDPPNGKCKRYHIFNDITSTEREDVENTLCCSSSSR--VAMSNY 120  
 DB 84 FLAIRGRNLVLEGYSDIYNG-KCRYRIFK-----SESDAETVCGDKSRPGTONNIPY 138

OY 121 NSLYPTMEKKAEVNSRNOVGIQLISSDIGK1 153  
 DB 139 EKSYKGMESKG--GARTKLGKIKTKLSRNGK1 169  
 RESULT 5  
 ID R1P6\_SAPOF STANDARD; PRT; 299 AA.  
 AC P20656: 041392;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-OCT-1996 (Rel. 34, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Ribosome-inactivating protein saporin-6 precursor (SAP-6) (SO-6)  
 DE (tRNA N-glycosidase) (EC 3.2.2.22).  
 GN SAP6.  
 OS Saponaria officinalis (Common soapwort).  
 OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllales: Caryophyllales: Saponariaceae: Saponaria.  
 OC NCBI\_TaxID=3572;  
 RN [1]  
 RP SEQUENCE OF 1-283 FROM N.A., AND SEQUENCE OF 25-115; 206-213 AND  
 RP 234-277.  
 RC TISSUE-Leaf;  
 RX MEDLINE=89338421; PubMed=2547612;  
 RA Benatti L., Saccardo M.B., Dani M., Nitli G., Sassano M.,  
 RA Lorenzetti R., Lappi D.A., Soria M.;  
 RT "Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-  
 RT inactivating protein from Saponaria officinalis.";  
 RL Eur. J. Biochem. 183:465-470(1989).  
 RN [2]  
 RP SEQUENCE OF 25-277 FROM N.A.  
 RX MEDLINE=93203250; PubMed=8454624;  
 RA Barthelmy J., Martineau D., Ong M., Matsunami R., Ling N.,  
 RA Benatti L., Cavallaro U., Soria M., Lappi D.A.;  
 RT "The expression of saporin, a ribosome-inactivating protein from the  
 RT plant Saponaria officinalis, in Escherichia coli.";  
 RL J. Biol. Chem. 268:6541-6548(1993).  
 RN [3]  
 RP SEQUENCE OF 275-299 FROM N.A.  
 RC TISSUE-Leaf;  
 RX MEDLINE=92038053; PubMed=1936274;  
 RA Benatti L., Nitli G., Solinas M., Valsasina B., Vitale A.,  
 RA Ceriotti A., Soria M.R.;  
 RT "A Saporin-6 cDNA containing a precursor sequence coding for a  
 RT carboxyl-terminal extension.";  
 RL FEBS Lett. 291:285-288(1991).  
 RN [4]  
 RP SEQUENCE OF 25-72 AND 114-154.  
 RX MEDLINE=90220515; PubMed=2325629;  
 RA Fordham-Skelton A.P., Yarwood A., Croy R.R.D.;  
 RT "Synthesis of saporin gene probes from partial protein sequence data:  
 RT use of inosine-oligonucleotides, genomic DNA and the polymerase chain  
 RT reaction.";  
 RL Mol. Gen. Genet. 221:134-138(1990).  
 CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS  
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR  
 CC PHARMACOLOGICAL APPLICATIONS.  
 CC -1- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- TISSUE SPECIFICITY: SEEDS AND LEAVES OF THE PLANT.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----

Query Match.	Best Local Similarity	70.6%: Score 559.5; DB 1; Length 294;
Matches 112: Conservative 16; Mismatches 22; Indels 3; Gaps 3		
QY 2 INTITFDAGNATINKYATFMESLRNOAKDPKLCYIGIMLPDPTNSTPKYLVLKLOGANLK 61		
DB 25 INTITFDGNNATINKYATFMKSIHQADPPLKCYIGIMLPDPTNLTPKYLVLTDSSSK 84		
QY 62 TITLMLRNNLTVMGYSDPFNGNCKRYHIFENDIT-STERTDVENTLCSSSSSRVAMSYNY 120		
DB 85 TITLMLKNNLTVMGYADTYNG-KCRYHIFKDISWTERNDVMTLLCPNPSRSGVGNKINY 143		
QY 121 NSLYPTMEKKAEVSRNOVQIGIQLSSDICKI 153		
DB 144 DSYPALEKKVG-RPRSOVQIGIQLNSGIGIKI 175		
RESULT 4		
RIP2_PHYAM	STANDARD:	PRT: 310 AA.
AC Q40772:		
16-Oct-2001 (Rel. 40, Created)		

RESULT 2  
 ID RIPL\_PHYAM STANDARD: PRT: 313 AA.  
 AC P10297;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-OCT-1993 (Rel. 27, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Antiviral protein I precursor (PAP-I) (PAP-C) (Ribosome-inactivating  
 protein) (rRNA N-glycosidase) (EC 3.2.2.22).  
 GN PAP1.  
 OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;  
 OC Caryophyllales: Caryophyllales: Phytolaccaceae; Phytolacca.  
 OC NCBI\_TaxID=3527;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-62.  
 RC TISSUE-Leaf;  
 RX MEDLINE=92003676; PubMed=1912488;  
 RA Lin O., Chen Z.C., Antoniw J.F., White R.F.;  
 RT "Isolation and characterization of a cDNA clone encoding the  
 RL anti-viral protein from Phytolacca americana.";  
 RN Plant Mol. Biol. 17:609-614(1991).  
 RP [2]  
 RP SEQUENCE OF 23-65.  
 RX MEDLINE=89193489; PubMed=2930487;  
 RA Barbieri L., Bolognesi A., Centini P., Falasca A.I., Minghetti A.,  
 RA Garofano L., Guicciardi A., Lappi D., Miller S.P.;  
 RT "Ribosome-inactivating proteins from plant cells in culture.";  
 RL Biochem. J. 257:801-807(1989).  
 RN [3]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Leaf;  
 RX MEDLINE=83290867; PubMed=6885760;  
 RA Houston L.L., Ramakrishnan S., Hermodson M.A.;  
 RT "Seasonal variations in different forms of pokeweed antiviral protein,  
 RL a potent inactivator of ribosomes.";  
 RN J. Biol. Chem. 258:9601-9604(1983).  
 RP [4]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Leaf;  
 RX MEDLINE=85023392; PubMed=6091760;  
 RA Born M.J., Larrick J., Platak M., Wilson K.J.;  
 RT "Characterization of translational inhibitors from Phytolacca  
 RT americana, amino-terminal sequence determination and antibody-  
 RL inhibitor conjugates.";  
 RN Biochim. Biophys. Acta 790:154-163(1984).  
 RP [5]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Root;  
 RX MEDLINE=91064383; PubMed=2248976;  
 RA Bolognesi A., Barbieri L., Abbondanza A., Falasca A.I., Carnicelli D.,  
 RA Bateilli M.G., Stirpe F.;  
 RT "Purification and properties of new ribosome-inactivating proteins  
 RT with RNA N-glycosidase activity.";  
 RL Biochim. Biophys. Acta 1087:293-302(1990).  
 RP [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=94016586; PubMed=8411176;  
 RA Monzinge A.F., Collins E.J., Ernst S.R., Irvin J.D., Robertus J.D.;  
 RT "The 2.5 A structure of pokeweed antiviral protein.";  
 RL J. Mol. Biol. 233:705-715(1993).  
 RP [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-284.  
 RX MEDLINE=99421320; PubMed=10493577;  
 RA Kurlinov I.V., Myers D.E., Irvin J.D., Uckun F.M.;  
 RT "X-ray crystallographic analysis of the structural basis for the  
 RT interactions of pokeweed antiviral protein with its active site  
 RT inhibitor and ribosomal RNA substrate analogs.";  
 RL Protein Sci. 8:1765-1772(1999).  
 CC -I- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN

CC SYNTHESIS IN VITRO.  
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -I- TISSUE SPECIFICITY: SPRING LEAVES AND ROOTS.  
 CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: X55383; CAA39054.1; -  
 DR PIR: S02792; S02792.  
 DR PIR: S13469; S13469.  
 DR PDB: 1PAF; 31-JAN-94.  
 DR PDB: 1PAG; 31-JAN-94.  
 DR PDB: 1OCI; 15-SEP-99.  
 DR PDB: 1OCG; 15-SEP-99.  
 DR PDB: 1OCJ; 15-SEP-99.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin; Signal; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 285  
 FT PROPEP 286 313  
 FT ACET\_SITE 198 198  
 FT DISULFID 56 281  
 FT DISULFID 107 128  
 FT STRAND 25 29  
 FT HELIX 35 49  
 FT STRAND 55 56  
 FT TURN 57 58  
 FT TURN 59 61  
 FT TURN 65 66  
 FT STRAND 71 78  
 FT HELIX 81 81  
 FT STRAND 82 89  
 FT TURN 90 93  
 FT STRAND 94 102  
 FT TURN 103 105  
 FT STRAND 106 112  
 FT TURN 113 114  
 FT TURN 117 117  
 FT HELIX 118 127  
 FT TURN 131 132  
 FT STRAND 134 136  
 FT STRAND 139 139  
 FT HELIX 145 152  
 FT TURN 153 153  
 FT TURN 157 158  
 FT STRAND 162 162  
 FT HELIX 164 174  
 FT TURN 175 176  
 FT HELIX 182 195  
 FT TURN 196 196  
 FT HELIX 197 201  
 FT HELIX 203 211  
 FT TURN 212 214  
 FT STRAND 217 217  
 FT HELIX 221 239  
 FT STRAND 241 241  
 FT TURN 242 243  
 FT STRAND 244 252  
 FT TURN 254 255  
 FT STRAND 258 263  
 FT HELIX 264 270



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:02 ; Search time 6.05346 Seconds  
(without alignments)  
1055.158 Million cell updates/sec

Title: US-09-978-274A-6  
Perfect score: 793  
Sequence: 1 MINTTFDAGNATINKYATF.....SRNOVQLOGIOLSSDIGKIS 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	667.5	84.2	261 1 RIPS_PHYAM	P23339 Phytolacca
2	596	75.2	313 1 RIPA_PHYAM	P10297 Phytolacca
3	559.5	70.6	294 1 RIPA_PHYAM	Q03464 Phytolacca
4	261	32.9	310 1 RIPA_PHYAM	Q40772 Phytolacca
5	191.5	24.1	299 1 RIPA_PHYAM	P20656 Saponaria o
6	184.5	23.3	253 1 RIPA_PHYAM	Q41389 Saponaria o
7	184.5	23.3	253 1 RIPA_PHYAM	Q41391 Saponaria o
8	183.5	23.1	292 1 RIPA_PHYAM	P27559 Saponaria o
9	169	21.3	293 1 RIPA_PHYAM	P24476 Dianthus ca
10	165.5	20.9	157 1 RIPA_PHYAM	P27661 Saponaria o
11	131	16.5	32 1 RIPA_PHYAM	P34867 Phytolacca
12	130.5	16.5	294 1 RIPA_PHYAM	P56526 Trichosanthe
13	124.5	15.7	236 1 RIPA_PHYAM	P27560 Saponaria o
14	123	15.5	286 1 RIPA_PHYAM	Q9474 Cucumis fig
15	122	15.4	527 1 RIPA_PHYAM	Q06077 abrus prec
16	120	15.1	278 1 RIPA_PHYAM	P21326 mibabialis j
17	118.5	14.9	286 1 RIPA_PHYAM	P16094 momordica c
18	118	14.9	250 1 RIPA_PHYAM	P22851 luffa cylin
19	115	14.5	563 1 NIGB_SAMI	P33183 Sambucus ni
20	111.5	14.1	282 1 RIPA_PHYAM	P98184 bryonia dio
21	111.5	14.1	289 1 RIPA_PHYAM	P24478 trichosanthe
22	111.5	14.1	290 1 RIPA_PHYAM	P33185 bryonia dio
23	111	14.0	576 1 RIPA_PHYAM	P02679 ricinus com
24	109.5	13.8	289 1 RIPA_PHYAM	P09989 trichosanthe
25	109.5	13.8	316 1 RIPA_PHYAM	P33186 gelonium mu
26	108	13.6	528 1 RIPA_PHYAM	P11140 abrus prec
27	100	12.6	562 1 RIPA_PHYAM	P28590 abrus prec
28	98.5	12.4	564 1 RIPA_PHYAM	P06750 ricinus com
29	96.5	12.2	286 1 RIPA_PHYAM	P29335 momordica b
30	87	11.0	319 1 RIPA_PHYAM	P09385 bacterioph
31	86	10.8	315 1 RIPA_PHYAM	P08026 bacterioph
32	85.5	10.8	280 1 RIPA_PHYAM	P22244 hordeum vul
33	85.5	10.8	280 1 RIPA_PHYAM	P04399 hordeum vul

34	85	10.7	254 1	MLA_VISAL	P81446 viscum albu
35	84.5	10.7	3343 1	YOST_CAEEL	P34616 caenohabdi
36	83	10.5	277 1	RIPA_LURCY	O00465 luffa cylin
37	83	10.5	315 1	SLTA_BP30	P10145 bacterioph
38	81.5	10.3	1528 1	TP2A_MOUSE	O01320 mus musculu
39	81	10.2	2875 1	RPL_TSWV1	P28976 tomato spot
40	79.5	10.0	235 1	PYRF_BABA	O44843 bartonella
41	79	10.0	300 1	RIP3_MAIZE	P25891 zea mays (m
42	79	10.0	1076 1	ROB_LASTIO	P27059 astasia jon
43	77.5	9.8	522 1	GD51_YEAST	P41913 saccharomyc
44	75	9.5	301 1	RIPX_MAIZE	P28522 zea mays (m
45	75	9.5	303 1	ALB3_MAIZE	P10593 zea mays (m

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	261 AA
RIPS_PHYAM	AC	P23339			
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Antiviral protein S (PAP-S) (Ribosome-inactivating protein) (rRNA				
OS	N-glycosidase) (EC 3.2.2.22).				
OC	Phytolacca americana (Common pokeweed) (Virginian pokeweed).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Caryophyllales; Caryophyllaceae; Phytolaccaceae; Phytolacca.				
OX	NCBI_TaxID=3527;				
RN	[1]				
RP	SEQUENCE:				
RC	TISSUE=Seed;				
RX	MEDLINE=91242096; PubMed=1368643;				
RA	Kung S.S., Kimura M., Funatsu G.;				
RT	"The complete amino acid sequence of antiviral protein from the seeds				
RT	of pokeweed (Phytolacca americana).";				
RL	Agric. Biol. Chem. 34:3301-3318(1990).				
CC	-1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN				
CC	SYNTHESIS IN VITRO.				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one				
CC	specific adenosine on the 28S rRNA.				
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.				
CC	TYPE 1 RIP SUBFAMILY.				
DR	PIR; J0401; J0401.				
DR	HSSP; Q03464; IAPA.				
DR	InterPro; IPR001574; RIP.				
DR	Pfam; PF00161; RIP. 1.				
DR	PRINTS; PR00396; SHIGARICIN.				
DR	PROSITE; PS00275; SHIGA_RICIN; 1.				
KW	Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolyase;				
KW	Toxin.				
FT	ACT_SITE 175 175 BY SIMILARITY.				
FT	DISULFID 34 258				
FT	DISULFID 84 105				
FT	SEQUENCE 261 AA; 29200 MW; D88B99962EB8399D CRC64;				
QY	Query Match	84.2%;	Score 667.5;	DB 1;	Length 261;
QY	Best Local Similarity	85.6%;	Pred. No. 7e-59;		
QY	Matches 111;	Conservative 9;	Mismatches 12;	Indels 1;	Gaps 1;
QY	2 INTTFDAGNATINKYATMESLRNOAKOPKLCYGI				
QY	1 INTTFDAGNATINKYATMESLRNOAKOPKLCYGI				
QY	62 TTLMRRNNLVYMGSDPENGKCRVHFNIDTSPERDV				
QY	61 TTLMRRNNLVYMGSDPYD-NKCRVHFNIDTSPERDV				
QY	122 SLVPTMEKRAEVSRRNOVQLOGIOLSSDIGKIS				
QY	120 GLVPTLEKRAGVTSRRNOVQLOGIOLSSDIGKIS				





N:Alternate names: ribosome-inactivating protein, saporin 2  
 C:Species: Saponaria officinalis (common soapwort)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1995  
 C:Accession: S29931  
 R:Sorta, M.R.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S28539  
 A:Accession: S29931  
 A:Molecule type: DNA  
 A:Residues: 1253 <SOR>  
 A:Cross-references: EMBL:X69135; NID:g21335; PIDN:CAA48889.1; PID:g21336  
 A:Experimental source: clone G-9  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase; monomer; toxin  
 F:6-249/Domain: RNA N-glycosidase homology <RNG>

	Query Match	24.0%	Score 190.5:	DB 2:	Length 253:
	Best Local Similarity	31.4%:	Pred No. 7.4e-11:		
	Matches	Conservative 50:	Mismatches 37:	Indels 11:	Gaps 5:
OY	2 INTITFDAGNATINKYAATFMEISLRNOADPKLKCYGIM-LPDTNSTPYKLVKLOGANL	60			
Dd	1 VTSTILDLVNPITPAQGYSSFFVDKIRNNVKDPLNKYCGTDIAVGPPSKKEFLINQSSR-	59			
OY	61 KTIITLMRLRNLLYWGSDPTNGNKR-YHIFNDITSTERPDVENTLCSSSSRYAAMSLN	119			
Dd	60 GTVISGLGRDLMLVVAYALAMANTIVNRAYVERSEITSLELT---ALPEATTANOKALE	115			
OY	120 YNSLYPTFEKKAEV---NSRNOVOLGIQLISDDIGAS	154			
Dd	116 YTDEDYSTEKNAQITOGDSCKKEIUGLGIDLLSTIMEAVN	154			

```

RESULT 10
S28539
rRNA N-glycosidase (EC 3.2.2.22) (clone G-1) - common soapwort (fragment)
N:Alternate names: ribosome-inactivating protein; saprotoxin
C:Species: Saponaria officinalis (common soapwort)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Aug-1999
C:Accession: S28539
R:Sorta, M.R.
submitted to the EMBL Data Library, October 1992
A:Reference number: S28539
A:Accession: S28539
A:Molecule type: DNA
A:Residues: 1_253 <SOR>
A:Cross-references: EMBL:X69131; NID:g21328; PIDN:CAA6885.1; PID:g21329
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycosidase; hydrolase; toxin
i:6-249/Domain: rRNA N-glycosidase homology <RNG>

```

	Query Match Similarity	23.3%	Score 184.5	DB 2:	Length 253:
	Best Local Similarity	30.8%	Pred. No. 2.8e-10:		
	Matches	49;	Conservative 37;	Mismatches 62;	Indels 11; Gaps 5
OY	2	INTITFDAGNATINKYATFMESLRNOAKDPKLCYGIPM-LPDTNSTPKYLVLVKGANL	60		
		: :   : : : :   : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
Db	1	VTSITLDLVNPFTAGYSFVDKIRNNVADPNLKCYGTDIADVIGPSKEFLINQSSR-	59		
OY	61	KTITLMERNLLYVMGYSDFPNGKCR-YHIFNDITSTERTDVENTLCCSSSRVAMSTN	119		
		: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
Db	60	GTVSLGLERDLNLVVAYALAMONTNVNRAYVFSEITSIELT---ALPEATTANOKALE	115		
OY	120	YNLSLYPTMEKKAAEV---NSRNVOVGIOIILSSDKGKS	154		
		: :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :			
Db	116	YTEDIYSTLEKNAOITGGDSKRRELGIDILLTLTSEAVN	154		

RESULT 11  
528542  
rRNA N-glycosidase (EC 3.2.2.22) (clone G-7) - common soapwort (fragment)  
N:Alternate names: ribosome-inactivating protein; saporin  
C:Species: *Saponaria officinalis* (common soapwort)

C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Aug-1999  
C:Accession: S28542  
R:Sorta: M.R  
Submitted to the EMBL Data Library, October 1992  
A:Reference number: S28533  
A:Accession: S28542  
A:Molecule type: DNA  
A:Residues: 1-253 <SOR>  
A:Cross-references: X69134: NID:g21333; PIDN:CAA4888.1; PID:g21334  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase; toxin  
F:6-249/Domain: rRNA N-glycosidase homology <RNG>

```

Query Match      23.3%  Score 184.5: DB 2: Length 253:
Best Local Similarity 30.8%: Pred. No. 2.8e-10:
Matches 49: Conservative 37: Mismatches 62: Indels 11: Gaps 5:

QY 2 INTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPTM-LPDTNSTPKYLLVLOGANL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 VTSITLDELVNTPAGQYSSFDKIRNNVNDPMLKYGQTFDIAVIGPPSKKEFLRINQSSR- 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 KTIILMLRRNLLYMGVSDPFGNGKCR-YHLENDITSTERFDVENTLCCSSSSSKVAMIN 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 GTVSLGLKRDMLLYVAYVLLAMDNTPVNNRAYVFRSEITSELTLP----ALPEATTANOKALE 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 120 YNSLYPTMEKKAEEV---NSRNOVOLGQIOLSSDICKIS 154
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 116 YTEDYQSTENKAQITIGCDKSKREELGGLGIDLLITISMEAVN 154
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 12  
S28541  
rRNA N-glycosidase (EC 3.2.2.22) (clone G-4) - common soapwort (fragment)  
N:Alternate names: ribosome inactivating protein; saporin  
C:Species: Saponaria officinalis (common soapwort)  
C:Date: 07-May-1993 #sequence-revision 07-May-1993 #text-change 20-Aug-1995  
C:Accession: S28541  
R:Soria, M.R.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S28539  
A:Accession: S28541  
A:Molecule type: DNA  
A:Residues: 1-253 <SOR>  
A:Cross-references: EMBL:X69133; NID:q21331; PIDN:CAA48887.1; PID:q21332  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase; toxin  
E:6-249/Domain: rRNA N-glycosidase homology <RNG>

[illegible]

RESULT 13  
RHOHG2  
tRNA N-glycosylase (EC 3.2.2.22) Sap2 precursor - common soapport  
N:Alternate names: ribosome-inactivating protein; saporin Z; saporin S5  
C:Species: Saponaria officinalis (common soapport)  
C:Date: 31-Mar-1993 #sequence,revision 31-Mar-1993 #text\_change 16-Jul-1999  
C:Accession: S17933, S28540, S38526, S15459  
R:Fordham-Skelton, A.P.; Taylor, P.N.; Hatley, M.R.; Croy, R.R.D.

Db 84 FTLAIRBGLYEGYSDIYNG-KCRYRIFKQ-----SEDAQETVCPGDKSKRGCTGNLIPY 138  
QY 121 NSLYPTMEKKAEVNSRNOVOLG:IOILSSDIGIKI 153  
Db 139 EKSYKGMESKG--GARTKLGLOKIRLKSRMGKI 169

RESULT 6  
Jc4811  
Beta vulgaris - beet  
C:Species: Beta vulgaris (beet)  
C:Date: 15-Aug-1996 #sequence\_revision 15-Oct-1996 #text\_change 20-Jun-2000  
C:Accession: Jc4811  
R:Horning, F.; Majant, H.; Jeske, H.; Mundry, K.W.  
Gene 170, 233-236, 1996  
A:Title: Cloning of a cDNA encoding a new ribosome-inactivating protein from Beta vulgaris  
A:Reference number: Jc4811; MUID:96235141; PMID:8666251  
A:Accession: Jc4811  
A:Molecule type: mRNA  
A:Residues: 1-272 <ORF>  
A:Cross-references: EMBL:X85567; NID:91405840; PIDN:CA5952.1; PID:91405841  
A:Note: The source is designated as Beta vulgaris vulgaris (mangold)  
C:Comment: This protein belongs to ribosome-inactivating protein type II.  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
F:28-271/Domain: rRNA N-glycosidase homology <RNG>

Query Match 24.3%; Score 192.5; DB 2; Length 272;  
Best Local Similarity 38.7%; Pred. No. 5.2e-11;  
Matches 55; Conservative 20; Mismatches 54; Indels 13; Gaps 5;

QY 5 ITFDAGNATINKYATFMESLRNOAKDPKLCYGIPLMDPTNTPRYLLVKLO----GANL 60  
Db 26 VTDEDTASKRYGVFLNRIYVDSKLYEGIMLPAPIKPARYLLAELAKKAGTDI 85  
QY 61 KTTTLMRLNNLYWGYSDPFNGNCRHYHENDITSTERTDVENTLCSSSSRVAMSIY 120  
Db 86 -TTTAAVKNDLYVAFLDQVAG-KLRAHYFDISLARAALPP-----ATQYIQIGY 137  
QY 121 NSLYPTMEKKAEVNSRNOVOLG 142  
Db 138 TSNYSIEGAAGSN-RVNFQLG 158

RESULT 7  
A58923  
rRNA N-glycosidase (EC 3.2.2.22) sapotin S9 - common soapwort  
C:Species: Saponaria officinalis (common soapwort)  
C:Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 01-Mar-2002  
C:Accession: A58923  
R:Mastrorcola, M.; Di Maro, A.; Ferranti, P.; Bolognesi, A.; Stipe, F.; Parente, A.  
Submitted to the Protein Sequence Database, December 1998  
A:Description: Sapotin-S9, the most basic ribosome-inactivating protein from Saponaria C  
A:Reference number: A58923  
A:Accession: A58923  
A:Molecule type: protein  
A:Residues: 1-253 <MAS>  
A:Experimental source: seeds  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase; toxin

Query Match 24.1%; Score 191.5; DB 2; Length 253;  
Best Local Similarity 32.1%; Pred. No. 5.9e-11;  
Matches 51; Conservative 36; Mismatches 61; Indels 11; Gaps 5;

QY 2 INTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLMDPTNTPRYLLVKLOANL 60  
Db 1 VTSITLIDLVPNTAGYSSFFVDKIRNNVDPNLKYGCTDIAIYGPSKSKFLRINQSSR- 59  
QY 61 KTTTLMRLNNLYWGYSDPFNGNCR-YHIFNDITSTERTDVENTLCSSSSRVAMSI 119  
Db 60 GTVSIGLKRDLNLYVAVYLAAMDNTNVRAYFRSEITSAELT----ALPPEATTAHAKALE 115

QY 120 YNSLYPTMEKKAEV-----NSRNOVOLG:IOILSSDIGIKS 154  
Db 116 YTEDYHSIEKNAQITEGDKSRKELGIGINLLSTMDTVN 154

RESULT 8  
S05205  
rRNA N-glycosidase (EC 3.2.2.22) 6 precursor - common soapwort (fragment)  
N:Alternate names: ribosome-inactivating protein SO-6; sapotin 6  
C:Species: Saponaria officinalis (common soapwort)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 20-Aug-1999  
C:Accession: S05205; A33231; S17689; S16330; A45499  
R:Benatti, L.; Saccardo, M.B.; Dani, M.; Nitti, G.; Sassano, M.; Lorenzetti, R.; Lapp  
Eur. J. Biochem. 183, 465-470, 1989  
A:Title: Nucleotide sequence of cDNA coding for sapotin-6, a type-1 ribosome-inactiva  
A:Reference number: S05205; MUID:89338421; PMID:2547612  
A:Accession: S05205  
A:Molecule type: mRNA  
A:Residues: 1-283 <BEN>  
A:Cross-references: EMBL:X15655  
A:Accession: A33231  
A:Molecule type: Protein  
A:Residues: 49-115;206-211,'T',213;234-277 <BEN2>  
R:Fordham-Skelton, A.P.; Yarwood, A.; Croy, R.R.D.  
Mol. Gen. Genet. 221, 134-138, 1990  
A:Title: Synthesis of sapotin gene probes from partial protein sequence data: use of  
A:Reference number: S11894; MUID:90220515; PMID:2325629  
A:Accession: S17689  
A:Molecule type: Protein  
A:Residues: 25-71,'D',77-88;102-122,'L',124-154 <FOR>  
R:Lappi, D.A.; Esch, F.S.; Barbieri, L.; Stipe, F.; Soria, M.  
Biochem. Biophys. Res. Commun. 129, 934-942, 1985  
A:Title: Characterization of a Saponaria officinalis seed ribosome-inactivating prote  
A:Reference number: S16330; MUID:85251709; PMID:3925952  
A:Accession: S16330  
A:Molecule type: Protein  
A:Residues: 25-41,'X',43-59,'S',61 <LAP>  
R:Barthelemy, I.; Martineau, D.; Ong, M.; Matsunami, R.; Ling, N.; Benatti, L.; Caval  
J. Biol. Chem. 268, 6541-6546, 1993  
A:Title: The expression of sapotin, a ribosome-inactivating protein from the plant Sa  
A:Reference number: A45499; MUID:93203250; PMID:8454624  
A:Accession: A45499  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 25-277 <BAR>  
A:Cross-references: GB:S57638; NID:9298762; PIDN:AAB25863.1; PID:9298763  
A:Note: sequence extracted from NCBI backbone (NCBIN:127937, NCBIPI:127934)  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase; monomer; toxin  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-283/Product: rRNA N-glycosidase 6 #status experimental <MAT>  
F:30-273/Domain: rRNA N-glycosidase homology <RNG>

Query Match 24.1%; Score 191.5; DB 2; Length 283;  
Best Local Similarity 31.4%; Pred. No. 6.8e-11;  
Matches 50; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 2 INTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLMDPTNTPRYLLVKLOANL 60  
Db 25 VTSITLIDLVPNTAGYSSFFVDKIRNNVDPNLKYGCTDIAIYGPSKSKFLRINQSSR- 83  
QY 61 KTTTLMRLNNLYWGYSDPFNGNCR-YHIFNDITSTERTDVENTLCSSSSRVAMSI 119  
Db 84 GTVSIGLKRDLNLYVAVYLAAMDNTNVRAYFRSEITSAEST----ALPPEATTAOKALE 139  
QY 120 YNSLYPTMEKKAEV-----NSRNOVOLG:IOILSSDIGIKS 154  
Db 140 YTEDYHSIEKNAQITEGDKSRKELGIGIDLLSTMEAVN 178

RESULT 9  
S29931  
rRNA N-glycosidase (EC 3.2.2.22) sapotin 2 (clone G-9) - common soapwort (fragment)



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 11.1384 Seconds

(Without alignments)  
1329.163 Million cell updates/sec

Title: US-09-978-274A-6  
Perfect score: 793  
Sequence: 1 MINTIFDAGNATINKYATF.....SRNQVLGIQLSSDGIKIS 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR-73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	667.5	84.2	261 2 JE0401	antiviral protein
2	396	75.2	313 2 S17757	rRNA N-glycosidase
3	559.5	70.6	294 2 S28421	rRNA N-glycosidase
4	278.5	35.1	289 2 T12573	rRNA N-glycosidase
5	261	32.9	310 2 S46239	ribosome-inactivat
6	192.5	24.3	272 2 JC4811	betavulgin - beet
7	191.5	24.1	253 2 A58823	rRNA N-glycosidase
8	191.5	24.1	253 2 S05205	rRNA N-glycosidase
9	190.5	24.0	253 2 S29931	rRNA N-glycosidase
10	184.5	23.3	253 2 S28539	rRNA N-glycosidase
11	184.5	23.3	253 2 S28542	rRNA N-glycosidase
12	183.5	23.1	253 2 S28541	rRNA N-glycosidase
13	183.5	23.1	292 1 R10MG2	rRNA N-glycosidase
14	169	21.3	293 2 S17519	rRNA N-glycosidase
15	165.5	20.9	157 2 S17934	rRNA N-glycosidase
16	131.5	16.6	245 2 JC4840	rRNA N-glycosidase
17	131	16.5	32 2 S38528	rRNA N-glycosidase
18	124.5	15.7	236 2 S17932	rRNA N-glycosidase
19	122	15.4	527 2 S32430	abrin-b precursor
20	120	15.1	278 2 A39617	rRNA N-glycosidase
21	118.5	14.9	286 1 R10PGC	rRNA N-glycosidase
22	118	14.9	250 2 JN0108	luffin-b - smooth
23	115	14.5	278 2 S23519	beta-luffin - smoo
24	111.5	14.1	247 2 J00393	karsurin - Mongol
25	111.5	14.1	247 2 JC5032	karsurin-B - Tric
26	111.5	14.1	289 2 JC5036	karsurin C - Tric
27	111	14.0	32 2 S32971	dodecandrin - endo
28	111	14.0	576 1 R1CSD	ricin D precursor
29	109.5	13.8	289 1 RLRTT	rRNA N-glycosidase

30	109.5	13.8	316 2 JT0753	rRNA N-glycosidase
31	108	13.6	528 1 TZLSA	abrin-a precursor
32	106.5	13.4	102 2 S11894	rRNA N-glycosidase
33	105.5	13.3	102 2 S17687	rRNA N-glycosidase
34	103.5	13.1	102 2 S17688	rRNA N-glycosidase
35	102	12.9	251 2 C39761	abrin (clone 7.2)
36	100	12.6	528 2 S32431	abrin-d precursor
37	100	12.6	562 2 S16022	abrin-c precursor
38	98.5	12.4	564 1 R1C5AG	agglutinin precurs
39	97.5	12.3	286 2 JC4235	rRNA N-glycosidase
40	96.5	12.2	286 2 S25560	rRNA N-glycosidase
41	91	11.5	319 2 I54695	shiga-like toxin I
42	88	11.1	319 2 S21940	hypothetical prote
43	87.5	11.0	821 2 C64461	hypothetical prote
44	87	11.0	319 2 E90779	shiga toxin 2 subu
45	87	11.0	319 2 G85640	shiga toxin 2 subu

#### ALIGNMENTS

RESULT 1  
JE0401  
antiviral protein - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C>Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 07-May-1999  
C:Accession: JE0401  
R:Kung, S.S.; Kimura, M.; Funatsu, G.  
A:Title: The complete amino acid sequence of antiviral protein from the seeds of pok  
A:Reference number: JE0401; MID:91242056; PMID:1368643  
A:Accession: JE0401  
A:Molecule type: Protein  
A:Residues: 1-261 <KUN>  
A:Experimental source: seed  
C:Comment: This protein prevents the replication of a number of plant viruses, and it  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: disulfide bond; glycoprotein  
F:6-254/Domain: rRNA N-glycosidase homology <RNG>  
F:10,44,255/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:34-258,84-105/Disulfide bonds: #status experimental

Query Match 84.2% Score 667.5; DB 2; Length 261;  
Best Local Similarity 85.6% Pred. No. 8.9e-57;  
Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKYATFMESLRNOAKPKLKGIGIPMLPTNTPKYLVLGQANLK 61  
|||||  
Db 1 INTITFDAGNATINKYATFMESLRNAKPKSLKCYGIPMLPTNSTITKILVLQASLK 60  
|||||

QY 62 TITLMLRNLLVYMGYSDFPENGKCRHYHFNITSTERTDVENTLCCSSSSRYAMSNYN 121  
|||||  
Db 61 TITLMLRNLLVYMGYSDFPDYD-NKCRHYHFNIDIKGTREYDVENTLCPSSNPVAKRTNYN 119  
|||||

QY 122 SLVPTMKKRAVSRNQVLGIQLSSDGIKIS 154  
|||||  
Db 120 GLVPLEKRAVTSRNEVOLGIQLSSDGIKIS 152  
|||||

RESULT 2  
S17757  
rRNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed  
N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-  
C:Species: Phytolacca americana (Virginian pokeweed)  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Aug-1999  
C:Accession: S17757; S02792; S13469; S32611  
R:Lin, Q.; Chen, Z.C.; Antoniw, J.F.; White, R.F.  
Plant Mol. Biol. 17, 609-614, 1991  
A:Title: Isolation and characterization of a cDNA clone encoding the anti-viral prote  
A:Reference number: S17757; MID:92003676; PMID:1912488  
A:Accession: S17757  
A:Molecule type: DNA  
A:Residues: 1-313 <LIN>

Wed Jul 2 12:19:00 2003

us-09-978-274a-8.ra1

Page 8

Search completed: July 2, 2003, 11:40:30  
Job time : 8.0912 secs

---



QY 62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYYNGTCQTT 110  
Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLINVTGCOAT 261

RESULT 14  
US-08-477-484B-9

Sequence 9, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-9

Query Match 75.4%; Score 429; DB 1; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;

Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPYKTEAFLLVAIQWVSEARPKYIENOVKTNFNRATYPPDPKVINLEEKWKIS 61  
Db 153 GCGSFTEKIEADFLVAIQWVSEARPKYIENOVKTNFNRDPSNDKVLDEENWKIST 212  
QY 62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYYNGTCQTT 110  
Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLINVTGCOAT 261

Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLINVTGCOAT 261

RESULT 15  
US-08-646-360-9

Sequence 9, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-9

Query Match 75.4%; Score 429; DB 2; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;

Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPYKTEAFLLVAIQWVSEARPKYIENOVKTNFNRATYPPDPKVINLEEKWKIS 61  
Db 153 GCGSFTEKIEADFLVAIQWVSEARPKYIENOVKTNFNRDPSNDKVLDEENWKIST 212  
QY 62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYYNGTCQTT 110  
Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLINVTGCOAT 261



```

COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988.430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-9

Query Match      75.4% Score 429; DB 1; Length 261;
Best Local Similarity 78.9% Pred. No. 3e-45;
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPVYKTEAFLLVATQVSEARFYKINOVKTNFRAPYDPKYNILEEKKGKISE 61
DB 153 GGGSTFEKIEADFLVLAQVSEARFYKINOVKTNFRDPSDKVLDLEENWGKIST 212
QY 62 AIHNAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKTVNGTCOTT 110
DB 213 AIHNSKNALPKPLELNADSTKWIVLRVDEIKPDVGLNVTGTCOAT 261

RESULT 10
US-08-425-336-9
Sequence 9, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425.336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6500
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-9

Query Match      75.4% Score 429; DB 1; Length 261;
Best Local Similarity 78.9% Pred. No. 3e-45;
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPVYKTEAFLLVATQVSEARFYKINOVKTNFRAPYDPKYNILEEKKGKISE 61
DB 153 GGGSTFEKIEADFLVLAQVSEARFYKINOVKTNFRDPSDKVLDLEENWGKIST 212
QY 62 AIHNAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKTVNGTCOTT 110
DB 213 AIHNSKNALPKPLELNADSTKWIVLRVDEIKPDVGLNVTGTCOAT 261

RESULT 11
US-08-378-761A-79
Sequence 79, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
```

Patent No. 5376546  
 Applicant: Bernhardt, Susan L  
 Applicant: Better, Marc D.  
 Applicant: Carroll, Steve F.  
 Applicant: Lane, Julie A.

```

1  GENERAL INFORMATION:
2  APPLICANT: Bernhard, Susan L.
3  APPLICANT: Better, Marc D.
4  APPLICANT: Carroll, Stephen F.
5  APPLICANT: Lane, Julie A.
6  APPLICANT: lei, Shau-Ping
7  TITLE OF INVENTION: Materials Comprising and Methods of
8  TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
9  NUMBER OF SEQUENCES: 101

```

ADDRESS: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Blokhell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois



TISSUE TYPE: Leaf  
US-08-373-858-2

Query Match 79.8%; Score 454; DB 1; Length 313;  
Best Local Similarity 82.6%; Pred. No. 3e-48;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Db 2 GVDSFPVKTEAFLLVAIQWSEARFYIENQVKTNNRAFYDDPKYINLEEKWKIS 61  
176 GVMSFTEKTEAFLLVAIQWSEARFYIENQVKTNNRAFPNPKYINLEETWGI 235

62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGSCOTT 110  
236 AIHDAKNGVLPKPLELDVDSAGAKWIVLRVDEIKPDVALLNYVGGSCOTT 284

RESULT 2  
US-08-500-611-2  
Sequence 2, Application US/08500611  
Patent No. 5756322  
GENERAL INFORMATION:  
APPLICANT: Tumer, Nilgun E.  
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500.611  
FILING DATE: 11-JUL-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
TELEX: 139-125  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-500-611-2

Query Match 79.8%; Score 454; DB 1; Length 313;  
Best Local Similarity 82.6%; Pred. No. 3e-48;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Db 2 GVDSFPVKTEAFLLVAIQWSEARFYIENQVKTNNRAFYDDPKYINLEEKWKIS 61  
176 GVMSFTEKTEAFLLVAIQWSEARFYIENQVKTNNRAFPNPKYINLEETWGI 235

62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGSCOTT 110  
236 AIHDAKNGVLPKPLELDVDSAGAKWIVLRVDEIKPDVALLNYVGGSCOTT 284

RESULT 3  
US-08-500-694-2  
Sequence 2, Application US/08500694  
Patent No. 880329  
GENERAL INFORMATION:

APPLICANT: Tumer, Nilgun E.  
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein Mutants  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500.694  
FILING DATE: 11-JUL-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
TELEX: 139-125  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-500-694-2

Query Match 79.8%; Score 454; DB 2; Length 313;  
Best Local Similarity 82.6%; Pred. No. 3e-48;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Db 2 GVDSFPVKTEAFLLVAIQWSEARFYIENQVKTNNRAFYDDPKYINLEEKWKIS 61  
176 GVMSFTEKTEAFLLVAIQWSEARFYIENQVKTNNRAFPNPKYINLEETWGI 235

62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGSCOTT 110  
236 AIHDAKNGVLPKPLELDVDSAGAKWIVLRVDEIKPDVALLNYVGGSCOTT 284

RESULT 4  
US-09-005-273-2  
Sequence 2, Application US/09005273  
Patent No. 6137030  
GENERAL INFORMATION:  
APPLICANT: Tumer, Nilgun E.  
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005.273  
FILING DATE: 09-JAN-1998

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: July 2, 2003, 11:37:03 ; Search time 7.0912 seconds

(without alignments)  
456.414 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569

Sequence: 1 MGVDSPFYKTEAFLLVAIQ.....DEINRDVALLKYNCTCQT 110

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents-AA.\*

1: /cgn2-6/ptodata/1/1aa/5A-COMB.pep.\*

2: /cgn2-6/ptodata/1/1aa/5B-COMB.pep.\*

3: /cgn2-6/ptodata/1/1aa/6A-COMB.pep.\*

4: /cgn2-6/ptodata/1/1aa/6B-COMB.pep.\*

5: /cgn2-6/ptodata/1/1aa/6C-COMB.pep.\*

6: /cgn2-6/ptodata/1/1aa/6D-COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	79.8	313	1 US-08-373-858-2	Sequence 2, Appli
2	454	79.8	313	1 US-08-500-611-2	Sequence 2, Appli
3	454	79.8	313	2 US-08-500-694-2	Sequence 2, Appli
4	454	79.8	313	4 US-09-005-273-2	Sequence 2, Appli
5	454	79.8	313	4 US-09-005-273-4	Sequence 4, Appli
6	454	79.8	313	5 PCT-US96-11546-2	Sequence 2, Appli
7	451	79.3	313	4 US-08-501-253A-2	Sequence 2, Appli
8	429	75.4	261	1 US-07-901-707-9	Sequence 9, Appli
9	429	75.4	261	1 US-07-988-430-9	Sequence 9, Appli
10	429	75.4	261	1 US-08-425-336-9	Sequence 9, Appli
11	429	75.4	261	1 US-08-378-761A-79	Sequence 79, Appli
12	429	75.4	261	1 US-08-485-286-79	Sequence 79, Appli
13	429	75.4	261	1 US-08-488-113B-9	Sequence 9, Appli
14	429	75.4	261	1 US-08-477-484B-9	Sequence 9, Appli
15	429	75.4	261	2 US-08-646-360-9	Sequence 9, Appli
16	429	75.4	261	4 US-08-839-765-9	Sequence 9, Appli
17	429	75.4	261	4 US-09-136-389-9	Sequence 9, Appli
18	429	75.4	261	4 US-09-610-838-9	Sequence 9, Appli
19	429	75.4	261	5 PCT-US92-09487-9	Sequence 9, Appli
20	399	70.1	305	1 US-08-138-636-2	Sequence 2, Appli
21	399	70.1	305	1 US-08-319-622A-2	Sequence 2, Appli
22	399	70.1	305	1 US-08-471-564-2	Sequence 2, Appli
23	213.5	37.5	251	1 US-08-425-336-109	Sequence 109, App
24	213.5	37.5	251	1 US-08-488-113B-109	Sequence 109, App
25	213.5	37.5	251	1 US-08-477-484B-109	Sequence 109, App
26	213.5	37.5	251	2 US-08-646-360-109	Sequence 109, App
27	213.5	37.5	251	4 US-08-839-765-109	Sequence 109, App

28	213.5	37.5	251	4 US-09-136-389-109	Sequence 109, App
29	213.5	37.5	251	4 US-09-610-838-109	Sequence 109, App
30	212.5	37.3	251	1 US-07-901-707-2	Sequence 2, Appli
31	212.5	37.3	251	1 US-08-425-336-2	Sequence 2, Appli
32	212.5	37.3	251	1 US-08-425-336-99	Sequence 99, Appli
33	212.5	37.3	251	1 US-08-425-336-101	Sequence 101, App
34	212.5	37.3	251	1 US-08-425-336-103	Sequence 103, App
35	212.5	37.3	251	1 US-08-425-336-106	Sequence 106, App
36	212.5	37.3	251	1 US-08-425-336-107	Sequence 107, App
37	212.5	37.3	251	1 US-08-425-336-108	Sequence 108, App
38	212.5	37.3	251	1 US-08-425-336-110	Sequence 110, App
39	212.5	37.3	251	1 US-08-488-113B-2	Sequence 2, Appli
40	212.5	37.3	251	1 US-08-488-113B-99	Sequence 99, Appli
41	212.5	37.3	251	1 US-08-488-113B-100	Sequence 100, App
42	212.5	37.3	251	1 US-08-488-113B-101	Sequence 101, App
43	212.5	37.3	251	1 US-08-488-113B-103	Sequence 103, App
44	212.5	37.3	251	1 US-08-488-113B-109	Sequence 109, App
45	212.5	37.3	251	1 US-08-488-113B-109	Sequence 109, App

## ALIGNMENTS

RESULT 1  
US-08-373-858-2  
Sequence 2, Application US/08373858

Patent No. 5633155

GENERAL INFORMATION:

APPLICANT: Kim, Man-Keun

APPLICANT: Lee, Kwan-Ho

APPLICANT: Na, Byeong-Kook

APPLICANT: Jeong, Han-Seung

APPLICANT: Choi, Kyu-Whan

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

TITLE OF INVENTION: Expression Vector for Phyto

TITLE OF INVENTION: Activiral Protein and Process for Preparing Transgenic

TITLE OF INVENTION: Plant Transformed Thereof.

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: US

ZIP: 10022-7513

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,858

FILING DATE: 18-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/17986-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-527-7770

TELEFAX: 212-753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Phytolacca americana

```

: GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: APPLICANT: Coggin, Philip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 73
: LENGTH: 332
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protein
: US-09-792-793A-73

```

```

Query Match          29.5%; Score 168; DB 9; Length 332;
Best Local Similarity 45.4%; Pred. No. 6.7e-11;
Matches 44; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

```

```

QY 8 VKTEAFFLLVAIQWSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIH-NA 66
DB 239 VKDEARFLLIAIQWSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIH-NA 298

```

```

QY 67 KNGALPKPLELVDAKGTWIVLRVDEINRDVALIKYV 103
DB 299 KNGVFNKDYDFGFK-----VRQVKDL--QWGLLWYL 328

```

```

RESULT 13
US-09-792-793A-76
: Sequence 76, Application US/09792793A
: Patent No. US20020168370A1
: GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: APPLICANT: Coggin, Philip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 76
: LENGTH: 332
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin Fusion Protein
: US-09-792-793A-76

```

```

Query Match          29.5%; Score 168; DB 9; Length 332;
Best Local Similarity 45.4%; Pred. No. 6.7e-11;
Matches 44; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

```

```

QY 8 VKTEAFFLLVAIQWSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIH-NA 66
DB 239 VKDEARFLLIAIQWSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIH-NA 298
QY 67 KNGALPKPLELVDAKGTWIVLRVDEINRDVALIKYV 103
DB 299 KNGVFNKDYDFGFK-----VRQVKDL--QWGLLWYL 328

```

```

RESULT 14
US-09-792-793A-36
: Sequence 36, Application US/09792793A
: Patent No. US20020168370A1
: GENERAL INFORMATION:

```

```

: APPLICANT: McDonald, John R.
: APPLICANT: Coggin, Philip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 36
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Momordica charantia
: US-09-792-793A-36

```

```

Query Match          25.9%; Score 147.5; DB 9; Length 250;
Best Local Similarity 39.2%; Pred. No. 9.7e-09;
Matches 38; Conservative 14; Mismatches 42; Indels 3; Gaps 1;

```

```

QY 8 VKTEAFFLLVAIQWSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIHNAK 67
DB 152 VKQAKFFLLVAIQWSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIHNAK 211
QY 68 ---NGLPKPLELVDAKGTWIVLRVDEINRDVALIK 101
DB 212 PSTTATKQCLATSPVITISPIWIKVEIKVLGLK 248

```

```

RESULT 15
US-09-792-793A-39
: Sequence 39, Application US/09792793A
: Patent No. US20020168370A1
: GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: APPLICANT: Coggin, Philip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 39
: LENGTH: 247
: TYPE: PRT
: ORGANISM: Trichosantheus kirilowii
: US-09-792-793A-39

```

```

Query Match          25.7%; Score 146; DB 9; Length 247;
Best Local Similarity 32.3%; Pred. No. 1.4e-08;
Matches 32; Conservative 22; Mismatches 41; Indels 4; Gaps 2;

```

```

QY 6 FPVTEAFFLLVAIQWSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIH-NA 64
DB 142 YNANSAASALWLIQSTSEARFKYIENQVKTNFRPFYPPPKYINLEEKWKISEAIIH-NA 201
QY 65 -NAKNGALPKPLELVDAKGTWIVLRVDEINRDVALIK 100
DB 202 ASTNNGOFESPFLVILNANONRVTTINVDAGVTSNAILL 240

```

```

Search completed: July 2, 2003, 12:00:37
Job time : 18.1226 secs

```





FILED DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 259:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 259:  
US-09-765-527-259

Query Match 37.3% Score 212.5; DB 10; Length 293;  
Best Local Similarity 44.7%; Pred. No. 5.3e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 3 VDSFVKTAEFLLVAIQWSEARFKYIENQVKTNFRAPYDPDKVINLEKWKISFA 62  
DB 167 IDNYKPTFIASSLLVVIQWSEARFTFIENQIRNNFOQIRPANNNTISLEKWKLSFQ 226  
QY 63 IH-NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALIKYVN 104  
DB 227 IRTSGANGMFESEAVELERANGKRYVYTAVDQVKPKIALLKFDV 269

US-09-765-527-253  
SEQUENCE 253, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 253:  
US-09-765-527-253

Query Match 37.3% Score 212.5; DB 10; Length 309;  
Best Local Similarity 44.7%; Pred. No. 5.7e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 3 VDSFVKTAEFLLVAIQWSEARFKYIENQVKTNFRAPYDPDKVINLEKWKISFA 62  
DB 167 IDNYKPTFIASSLLVVIQWSEARFTFIENQIRNNFOQIRPANNNTISLEKWKLSFQ 226  
QY 63 IH-NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALIKYVN 104  
DB 227 IRTSGANGMFESEAVELERANGKRYVYTAVDQVKPKIALLKFDV 269

US-09-765-527-251  
SEQUENCE 251, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 251:  
US-09-765-527-251

Query Match 37.3% Score 212.5; DB 10; Length 332;  
Best Local Similarity 44.7%; Pred. No. 6.2e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 3 VDSFVKTAEFLLVAIQWSEARFKYIENQVKTNFRAPYDPDKVINLEKWKISFA 62  
DB 167 IDNYKPTFIASSLLVVIQWSEARFTFIENQIRNNFOQIRPANNNTISLEKWKLSFQ 226  
QY 63 IH-NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALIKYVN 104  
DB 227 IRTSGANGMFESEAVELERANGKRYVYTAVDQVKPKIALLKFDV 269

APPLICANT: McPherson, Michael  
APPLICANT: Atkinson, Howard  
APPLICANT: Neelam, Anil  
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM  
FILE REFERENCE: 9341-028  
CURRENT APPLICATION NUMBER: US/09/978,274A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0025225.4  
PRIOR FILING DATE: 2000-10-14  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 4  
LENGTH: 263  
TYPE: PRT  
ORGANISM: Phytolacca americana  
US-09-978-274A-4

Query Match 99.1%; Score 564; DB 10; Length 263;  
Best Local Similarity 100.0%; Pred. No. 7.9e-56;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GVDSPVKTAEFLFLVAIQWSEARFKYIENOVKTENFRAPFPDPKVINLEEKWKISE 61  
DB 155 GVDSPVKTAEFLFLVAIQWSEARFKYIENOVKTENFRAPFPDPKVINLEEKWKISE 214  
OY 62 AHNNAKGALEPKLELVDAKGTWKIVLRDEINRDVALLKYVNGTCOTT 110  
DB 215 AHNNAKGALEPKLELVDAKGTWKIVLRDEINRDVALLKYVNGTCOTT 263

RESULT 3  
US-09-978-274A-2  
Sequence 2, Application US/09978274A  
Patent No. US20020116737A1  
GENERAL INFORMATION:  
APPLICANT: Thomas, Christopher  
APPLICANT: McPherson, Michael  
APPLICANT: Atkinson, Howard  
APPLICANT: Neelam, Anil  
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM  
FILE REFERENCE: 9341-028  
CURRENT APPLICATION NUMBER: US/09/978,274A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0025225.4  
PRIOR FILING DATE: 2000-10-14  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 2  
LENGTH: 314  
TYPE: PRT  
ORGANISM: Phytolacca americana  
US-09-978-274A-2

Query Match 99.1%; Score 564; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 9.9e-56;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GVDSPVKTAEFLFLVAIQWSEARFKYIENOVKTENFRAPFPDPKVINLEEKWKISE 61  
DB 178 GVDSPVKTAEFLFLVAIQWSEARFKYIENOVKTENFRAPFPDPKVINLEEKWKISE 237  
OY 62 AHNNAKGALEPKLELVDAKGTWKIVLRDEINRDVALLKYVNGTCOTT 110  
DB 238 AHNNAKGALEPKLELVDAKGTWKIVLRDEINRDVALLKYVNGTCOTT 286

RESULT 4  
US-09-765-527-247  
Sequence 247, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of

NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 247:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 247:  
US-09-765-527-247

Query Match 37.3%; Score 212.5; DB 10; Length 251;  
Best Local Similarity 44.7%; Pred. No. 4.3e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

OY 3 VDSFPVKTAEFLFLVAIQWSEARFKYIENOVKTENFRAPFPDPKVINLEEKWKISE 62  
DB 145 INYKPTETIASLLVLIQWSEARFTIENQIRNFRANNTISLEKWKISLFO 204  
OY 63 IHNNAKGALEPKLELVDAKGTWKIVLRDEINRDVALLKYV 104  
DB 205 IRTSGANGHSEAEVLELRANGKKYVTAVDQYKRIALLKFPD 247

RESULT 5  
US-09-765-527-259  
Sequence 259, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:40:38 ; Search time 17.1226 Seconds

(Without alignments)  
738.742 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569

Sequence: 1 MGVDSFPVKTEAFFLLVAIQ.....DEINRDVALLKYVNGTCOTT 110

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications-AA\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US60\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	569	100.0	110	10	US-09-978-274A-8	Sequence 8, Appli
2	564	99.1	263	10	US-09-978-274A-4	Sequence 4, Appli
3	564	99.1	314	10	US-09-978-274A-2	Sequence 2, Appli
4	212.5	37.3	251	10	US-09-765-527-247	Sequence 247, App
5	212.5	37.3	293	10	US-09-765-527-259	Sequence 259, App
6	212.5	37.3	309	10	US-09-765-527-253	Sequence 253, App
7	212.5	37.3	332	10	US-09-765-527-251	Sequence 251, App
8	168	29.5	254	9	US-09-792-793A-85	Sequence 85, Appli
9	168	29.5	275	9	US-09-792-793A-35	Sequence 35, Appli
10	168	29.5	327	9	US-09-792-793A-79	Sequence 79, Appli
11	168	29.5	330	9	US-09-792-793A-82	Sequence 82, Appli
12	168	29.5	332	9	US-09-792-793A-76	Sequence 76, Appli
13	168	29.5	332	9	US-09-792-793A-36	Sequence 36, Appli
14	147.5	25.9	247	9	US-09-792-793A-39	Sequence 39, Appli
15	146	25.7	252	10	US-09-347-064-2	Sequence 2, Appli
16	132	23.2	252	10	US-09-347-064-8	Sequence 8, Appli
17	132	23.2	247	9	US-09-792-793A-34	Sequence 34, Appli
18	129	22.7	1447	10	US-09-797-097-2	Sequence 2, Appli
19	85.5	15.0				

20	79	13.9	1024	9	US-10-211-962-84	Sequence 84, Appli
21	77.5	13.6	1454	10	US-09-854-799-22	Sequence 22, Appli
22	77.5	13.6	1454	10	US-09-854-799-26	Sequence 26, Appli
23	77.5	13.6	1454	10	US-09-854-799-32	Sequence 32, Appli
24	76.5	13.4	1101	10	US-09-972-484-52	Sequence 52, Appli
25	76.5	13.4	1101	10	US-09-972-484-54	Sequence 54, Appli
26	76.5	13.4	1452	10	US-09-972-484-2	Sequence 2, Appli
27	74	13.0	1024	9	US-10-211-962-81	Sequence 81, Appli
28	70.5	12.4	251	10	US-09-972-484-59	Sequence 59, Appli
29	70	12.3	1024	9	US-10-211-962-83	Sequence 83, Appli
30	69.5	12.2	798	10	US-09-861-451A-12	Sequence 12, Appli
31	69	12.1	763	10	US-09-861-451A-12	Sequence 12, Appli
32	68	12.0	1024	9	US-10-211-962-88	Sequence 88, Appli
33	66	11.6	250	9	US-09-802-208B-3	Sequence 3, Appli
34	66	11.6	730	10	US-09-815-242-10741	Sequence 10741, A
35	65.5	11.5	2789	10	US-09-801-574-57	Sequence 57, Appli
36	64.5	11.3	249	9	US-10-153-668-118	Sequence 118, Appli
37	64.5	11.3	306	9	US-10-153-668-120	Sequence 120, Appli
38	64.5	11.3	365	9	US-09-809-391-696	Sequence 696, Appli
39	64	11.2	638	9	US-10-309-437-4	Sequence 4, Appli
40	64	11.2	1024	9	US-10-211-962-86	Sequence 86, Appli
41	63.5	11.2	380	10	US-09-977-653-8	Sequence 8, Appli
42	63.5	11.2	432	9	US-09-746-660A-102	Sequence 102, Appli
43	63.5	11.2	432	10	US-09-977-653-6	Sequence 6, Appli
44	63.5	11.2	474	9	US-09-738-626-4336	Sequence 4336, Appli
45	63.5	11.2	475	10	US-09-738-363-8	Sequence 8, Appli

# ALIGNMENTS

```

RESULT 1
US-09-978-274A-8
; Sequence 8, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-09-978-274A-8

Query Match      100.0%; Score 569; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 6,7e-57;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVDSFPVKTEAFFLLVAIQWSEAFKRYLENQVKTNFNRAFYDDPKVINLEEKWGIS 60
    |||||||
Db 1 MGVDSFPVKTEAFFLLVAIQWSEAFKRYLENQVKTNFNRAFYDDPKVINLEEKWGIS 60

QY 61 EAIHNAKGALEPKLELDVDAKGTWIVLRVDEINRDVALLKYVNGTCOTT 110
    |||||||
Db 61 EAIHNAKGALEPKLELDVDAKGTWIVLRVDEINRDVALLKYVNGTCOTT 110

RESULT 2
US-09-978-274A-4
; Sequence 4, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher

```

PT - New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
xx

Claim 8; -; 64pp; English.

Protein AAW14163-N14265 represent new pokeweed antiviral protein (PAP) mutants having reduced phytotoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-N14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. Prior to processing, the protein contains a 22 amino acid N-terminal signal sequence and a 29 amino acid C-terminal extension. PAP is a Type I ribosomal inhibitor protein (RIP) that catalyses the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can confer broad spectrum virus and fungus resistance to plants without causing plant cell death or sterility. They can also confer increased resistance to insects, bacteria and nematodes in plants. C.N.B. This sequence is not given in the specification but is generated from the wild type sequence reproduced in the specification.

Sequence 189 AA;

Query Match	75.28;	Score 596;	DB 18;	length 189;
Best Local Similarity	71.98;	Pred. No. 8.7e-60;		
Matches 110;	Conservative 23;	Mismatches 20;	Indels 0;	Gaps 0;

[illegible]

```
Search completed: July 2, 2003, 11:39:41
Job time : 28.088 secs
```



```

DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal.
KM Multigene family.
FT SIGNAL 1 24
FT CHAIN 25 292
FT ACT_SITE 200 200
FT VARIANT 72 72 D -> E.
SQ SEQUENCE 292 AA; 32810 MW; FA143CE01BE8976 CRC64;

Query Match 30.2%; Score 170.5; DB 1; Length 292;
Best Local Similarity 41.0%; Pred. No. 1.6e-10;
Matches 47; Conservative 12; Mismatches 37; Indels 17; Gaps 4;

OY 7 VKTEAFLLVAIOMVSEARFKYIENQVKNFRAFPDPKVINLEKCKISEAH-N 65
Db 184 VKNEARFLLAIOMTAEVAFRIYONLVKNFKNKDSNKKYQFEVSNRKISTAIYGD 243
OY 66 KNGALPKLELVDAKGTWIVLRVDEINRDVALLKVV-----NGTCOTT 109
Db 244 KNGVFNKDYDFGFK-----VROVKDL--QMGLMYLKGPKSSNEANSTAYAT 289

RESULT 10
RIP1_TRIAN STANDARD; PRT; 294 AA.
AC P56626; O2QOY7;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type I ribosome-inactivating protein trichoangulina precursor (rRNA
DE N-glycosidase) (EC 3.2.2.22) (RIP) (Trichoangulin).
GN TCA.
OS Trichosanthes angulina (Snake gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=50544;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=cv. Angina; TISSUE=Seed;
RX MEDLINE=99132006; PubMed=991318;
RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,
RA Lin J.-Y.;
RT "Purification, characterization and molecular cloning of trichoangulin,
RT a novel type I ribosome-inactivating protein from the seeds of
RT Trichosanthes angulina.";
RL Biochem. J. 338:211-219(1999).
RN [2]
RP SEQUENCE OF 20-264.
RC TISSUE=Seed;
RA Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;
RT "Amino acid sequence of trichoangulina, a ribosomal-inactivating
RT protein from Trichosanthes angulina seeds.";
RL J. Biomed. Sci. 3:1178-186(1996).
-1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN
CC RIBOSOMES.
-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
EMBL AF055086; AM02686.1; -

```

```

DR HSSP: P33185; 1BRV.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN. FALSE_NEG.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin.
KM Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 264
FT PROPER 265 294
FT ACT_SITE 177 177
FT ACT_SITE 180 180
FT CARBOHYD 70 70
FT CARBOHYD 220 220
FT CONFLICT 51 51 C -> Y (IN REF. 2).
FT CONFLICT 65 65 W -> R (IN REF. 2).
FT CONFLICT 84 84 N -> D (IN REF. 2).
FT CONFLICT 152 152 A -> S (IN REF. 2).
FT CONFLICT 174 174 C -> S (IN REF. 2).
FT CONFLICT 245 245 N -> H (IN REF. 2).
SQ SEQUENCE 294 AA; 32234 MW; DAAFB87CE3290994 CRC64;

Query Match 30.2%; Score 170.5; DB 1; Length 294;
Best Local Similarity 38.2%; Pred. No. 1.6e-10;
Matches 39; Conservative 20; Mismatches 38; Indels 5; Gaps 2;

OY 5 FPKVTEAFLLVAIOMVSEARFKYIENQVKNFRAFPDPKVINLEKCKISEAH-N 64
Db 159 YDYOSTAALVLVLIQCTAAARAKYIEQVSSHISNFPNVAIVSLKMGALSQIOI 218
OY 65 AK---NGALPKLELVDAKGTWIVLRVDE--INRDVALLK 101
Db 219 AARTGCGQENVELYNPDGTRFSTNIGAVGNKIKLLY 260

RESULT 11
RIP5_SAPOF STANDARD; PRT; 253 AA.
AC Q41389;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-5 (EC 3.2.2.22) (SAP-5) (rRNA N-
DE glycosidase).
GN SAP5.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=93203250; PubMed=8454624;
RA Barthelemy I., Martineau D., Ong M., Matsumami R., Ling N.,
RA Benatti L., Cavallaro U., Sorio M., Lapi D.A.;
RT "The expression of saporin, a ribosome-inactivating protein from the
RT plant Saponaria officinalis, in Escherichia coli.";
RL J. Biol. Chem. 268:6541-6548(1993).
-1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

DR EMBL: X69131: CAA48885.1: -  
 DR EMBL: X69132: CAA48886.1: -  
 DR HSSP: P10297: IOCG.  
 DR InterPro: IPR001574: RIP.  
 DR Pfam: PF00161: RIP: 1.  
 DR PROSITE: PS00275: SHIGA-RICIN: 1.  
 KW Plant defense: Protein synthesis inhibitor: Hydrolase: Toxin:  
 MultiGene family.  
 FT ACT\_SITE 176: 176 BY SIMILARITY.  
 SQ SEQUENCE 253 AA: 28556 MW: 5396935E13D0E994D CRC64;  
 Query Match 30.1%; Score 170; DB 1; Length 253;  
 Best Local Similarity 45.4%; Pred. No. 1.5e-10;  
 Matches 44: Conservative 12: Mismatches 33: Indels 8: Gaps 3:

QY 7 VKTEAFLLVAIOMSEARFKYIENQVKTNFNRAFYDDPKVINLEEKGRISEAIIH-NA 65  
 ID RIP6\_SAPOF STANDARD: PRT: 253 AA.  
 AC Q41391.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein saporin-7 (SO-7) (SAP-7) (rRNA N-  
 glycosidase) (EC 3.2.2.22).  
 GN SAP7.  
 OS Saponaria officinalis (Common soapwort).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllales: Caryophyllaceae: Saponaria.  
 RX NCBI\_TaxID=3572;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=93203250; PubMed=8454624;  
 RA Barthelmy I., Martineau D., Ong M., Matsunami R., Ling N.,  
 RA Benatti L., Cavallaro U., Soria M., Lappi D.A.:  
 "The expression of saporin, a ribosome-inactivating protein from the  
 plant *Saponaria officinalis*, in *Escherichia coli*.";  
 RT J. Biol. Chem. 268:6541-6548(1993).  
 RL [3]  
 CC - FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS  
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).  
 CC - CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X69134: CAA48888.1: -  
 DR HSSP: P10297: IOCG.  
 DR InterPro: IPR001574: RIP.  
 DR Pfam: PF00161: RIP: 1.  
 DR PROSITE: PS00275: SHIGA-RICIN: 1.  
 DR Plant defense: Protein synthesis inhibitor: Hydrolase: Toxin:  
 KW MultiGene family.  
 FT ACT\_SITE 176 176 BY SIMILARITY.

SQ SEQUENCE 253 AA: 28553 MW: 161319102AB20539 CRC64;  
 Query Match 30.0%; Score 169; DB 1; Length 253;  
 Best Local Similarity 45.4%; Pred. No. 1.9e-10;  
 Matches 44: Conservative 13: Mismatches 32: Indels 8: Gaps 3:

QY 7 VKTEAFLLVAIOMSEARFKYIENQVKTNFNRAFYDDPKVINLEEKGRISEAIIH-NA 65  
 ID RIP6\_SAPOF STANDARD: PRT: 299 AA.  
 AC P20656: Q41392.  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein saporin-6 precursor (SAP-6) (SO-6)  
 DE (rRNA N-glycosidase) (EC 3.2.2.22).  
 GN SAP6.  
 OS Saponaria officinalis (Common soapwort).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllales: Caryophyllaceae: Saponaria.  
 RX NCBI\_TaxID=3572;  
 RN [1]  
 RP SEQUENCE OF 1-283 FROM N.A., AND SEQUENCE OF 25-115: 206-213 AND  
 RP 234-277.  
 RC TISSUE=Leaf;  
 RX MEDLINE=89338421; PubMed=2547612;  
 RA Benatti L., Saccardo M.B., Dani M., Nitli G., Sassano M.,  
 RA Lorenzetti R., Lappi D.A., Soria M.:  
 "Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-  
 RT inactivating protein from *Saponaria officinalis*.";  
 RL Eur. J. Biochem. 183:465-470(1989).  
 RN [2]  
 RN [3]  
 RP SEQUENCE OF 25-277 FROM N.A.  
 RX MEDLINE=93203250; PubMed=8454624;  
 RA Barthelmy I., Martineau D., Ong M., Matsunami R., Ling N.,  
 RA Benatti L., Cavallaro U., Soria M., Lappi D.A.:  
 "The expression of saporin, a ribosome-inactivating protein from the  
 plant *Saponaria officinalis*, in *Escherichia coli*.";  
 RT J. Biol. Chem. 268:6541-6548(1993).  
 RL [3]  
 CC - FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS  
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR  
 CC PHARMACOLOGICAL APPLICATIONS.  
 CC - CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC - TISSUE SPECIFICITY: SEEDS AND LEAVES OF THE PLANT.  
 CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.



CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))

DR EMBL: X15655; CAA33685.1; -  
DR EMBL: S57638; AAB25863.1; -  
DR EMBL: X69135; CAA48889.1; -  
DR EMBL: X64917; CAA46110.1; -  
DR EMBL: A00352; CAA00055.1; -  
DR PIR: S05205; S05205.  
DR HSR: P10297; 10CG.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA.RICIN.  
DR Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin; Signal;  
KW Multigene family.  
FT SIGNAL 1 24  
FT CHAIN 25 277 RIBOSOME-INACTIVATING PROTEIN SAPORIN-6.  
FT PROPEP 278 299 POTENTIAL.  
FT ACT\_SITE 200 200 BY SIMILARITY.  
FT CAROHD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 72 72 E -> D.  
FT VARIANT 115 115 S -> K.  
FT CONFLICT 123 123 S -> L (IN REF. 2 AND 4).  
FT CONFLICT 212 212 I -> T (IN REF. 1; AA SEQUENCE).  
SQ SEQUENCE 299 AA: 33607 MW: 48C312958BB4E79B CRC64;

Query Match 29.8%; Score 168; DB 1; Length 299;  
Best Local Similarity 45.4%; Pred. No. 2.9e-10;  
Matches 44; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

OY 7 VKTEAFLLVIAOMSEARFKYIENOVKTNFRATYDDPKYINLEEKWKISSEAIH-NA 65  
DB 184 VKDEARFLIATOMSEARFKYIENOVKTNFRATYDDPKYINLEEKWKISSEAIH-NA 243-  
OY 66 KNGALPKLELVDAKGTQWIVLRVDEINRDVALLKYV 102  
DB 244 KNGVFNKDYDFGFGK-----VRQVKDL--QMGGLMYL 273

RESULT 14  
RIP2\_BRYDI STANDARD: PRT: 282 AA.  
ID RIP2\_BRYDI  
AC P98184; O9S830;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BD2).  
OS Bryonia dioica (Red bryony).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucotsids I; Cucurbitales; Cucurbitaceae; Bryonia.  
OX NCBI\_TaxID=3652;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stegall C.B., Gawlak S.L., Marguardt H.,  
RT "Bryodin 2 a ribosome-inactivating protein isolated from the plant Bryonia dioica."  
RL Patent number US5597569, 28-JAN-1997.  
RN [2]  
RP SEQUENCE OF 22-42.  
RC TISSUE=Root;  
RX MEDLINE=95151812; PubMed=7849072;  
RA Stegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B., Marguardt H.;  
RT "Characterization of ribosome-inactivating proteins isolated from

RT Bryonia dioica and their utility as carcinoma-reactive  
RT immunocytogenetics.";  
RL Bioconj. Chem. 5:423-429(1994).  
CC - FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS  
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).  
CC - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))

DR EMBL: X34238; -; NOT\_ANNOTATED\_CDS.  
DR HSR: P09989; 1MRJ.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA.RICIN.  
DR Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;  
KW Multigene family; Glycoprotein; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.  
FT ACT\_SITE 183 183 BY SIMILARITY.  
FT CAROHD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 282 AA: 30754 MW: C52BE2F6A873769C CRC64;

Query Match 29.3%; Score 165.5; DB 1; Length 282;  
Best Local Similarity 42.2%; Pred. No. 5e-10;  
Matches 38; Conservative 13; Mismatches 36; Indels 3; Gaps 2;

OY 15 LVATOMSEARFKYIENOVKTNFRATYDDPKYINLEEKWKISSEAIHNA-KNGALPK 72  
DB 175 LVIIQTVEARFKYIENOVKTNFRATYDDPKYINLEEKWKISSEAIHNA-KNGALPK 234  
OY 73 PLELVDAKGTQWIVLRVDEINRDVALLKY 101  
DB 235 PVELRTVSNTPFTVNVSPYKGIALLLY 264

RESULT 15  
RIP0\_DICA STANDARD: PRT: 293 AA.  
ID RIP0\_DICA  
AC P24476; 01-MAR-1992 (Rel. 21, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Antiviral protein DAP-30 precursor (Ribosome-inactivating protein) (rRNA N-glycosidase) (EC 3.2.2.22) (Dianthin 30).  
OS Dianthus caryophyllus (Carnation) (Clove pink).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Dianthus.  
OX NCBI\_TaxID=3570;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=9135219; PubMed=1840496;  
RA Legname G., Bellosta P., Gromo G., Modena D., Keen J.N., Roberts L.M., Lord J.M.;  
RT "Nucleotide sequence of cDNA coding for dianthin 30, a ribosome inactivating protein from Dianthus caryophyllus."  
RL Biochim. Biophys. Acta 1090:119-122(1991).  
RN [2]  
RP SEQUENCE OF 24-82.  
RC TISSUE=Leaf;  
RX MEDLINE=92037998; PubMed=1936243;  
RA Lee-Huang S., Kung H.-F., Huang P.L., Huang P.L., Li B.-Q., Huang P., Huang H.-I., Chen H.-C.;

```

RT      "A new class of anti-HIV agents: GAP31, DAPs 30 and 32."
RL      FEBS Lett. 291:139-144(1991).
CC      -1- FUNCTION: SINGLE-CHAIN RIBOSOME-INACTIVATING PROTEIN, POSSESSING
CC      HIGH ANTIVIRAL POTENCY AND LOW TOXICITY TO NORMAL CELLS IN CULTURE
CC      AND TO INTRACT ANIMALS. CAPABLE OF INHIBITING HIV-1 INFECTION AND
CC      REPLICATION.
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC      TYPE 1 RIP SUBFAMILY.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL: X59260; CAA41953.1; ALT_SEQ.
CC      PIR: S17519; S17519.
CC      DR      HSSP: 003464; IAPA.
CC      DR      InterPro: IPR001574; RIP.
CC      DR      Pfam: PF00161; RIP; 1.
CC      DR      PRINTS: PR00396; SHIGARICIN.
CC      DR      PROSITE: PS00275; SHIGA_RICIN; 1.
CC      KW      Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
CC      Toxin; Signal.
CC      FT      SIGNAL      1      23
CC      FT      CHAIN      24      293
CC      FT      ACT_SITE    200      200
CC      SQ      SEQUENCE    293 AA: 32717 MW: AC85AAC8725DAF2 CRC64;
-----
Query Match      28.9%; Score 163; DB 1; Length 293;
Best Local Similarity 43.3%; Pred.No.9.5e-10;
Matches 42; Conservative 13; Mismatches 34; Indels 8; Gaps 3;

```

```

OY      7 VKTEAFFLLVAIQWSEARFKYIENOVKTENFRAPYPPDKVINLEKMGKISEAH-NA 65
DB      184 VKDEARFLLAIQMTAEARFRIOQLYKFNPKRDESENKYIQFOVSMKISTALFGDC 243
OY      66 KNGALPKPLELVDAKGTWIVLRVDEINRDVALKXY 102
DB      244 KNGVENKDYDFGFGK-----VRQAKDL--QMGLLKYL 273

```

Search completed: July 2, 2003, 11:37:38  
 Job time : 5.28459 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 7.95598 Seconds

(without alignments)  
1329.163 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569

Sequence: 1 MGVDSPVKTAEAFLLVAIQ.....DEINRDVALLKVVNGTCQTT 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_73:\*\*

1: PIR1:\*\*

2: PIR2:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	457	80.3	294	2	S28421	rRNA N-glycosidase
2	454	79.8	313	2	S17757	rRNA N-glycosidase
3	429	75.4	261	2	JE0401	antiviral protein
4	215	37.8	272	2	JC4811	betavirgin - beet
5	213.5	37.5	316	2	UT0753	rRNA N-glycosidase
6	200	35.1	310	2	S46739	ribosome-inactivat
7	192	33.7	564	1	RLCSAG	agglutinin precursor
8	192	33.7	576	1	RLCSAG	ricin D precursor
9	176	30.9	236	2	S17932	rRNA N-glycosidase
10	171.5	30.1	253	2	A58923	rRNA N-glycosidase
11	170.5	30.0	245	2	JC4840	rRNA N-glycosidase
12	170.5	30.0	292	1	RL0HG2	rRNA N-glycosidase
13	170	29.9	253	2	S28541	rRNA N-glycosidase
14	170	29.9	253	2	S28539	rRNA N-glycosidase
15	169	29.7	253	2	S28542	rRNA N-glycosidase
16	168	29.5	253	2	S29931	rRNA N-glycosidase
17	168	29.5	253	2	S05205	rRNA N-glycosidase
18	163	28.6	293	2	S17519	rRNA N-glycosidase
19	149	26.2	289	2	T12573	rRNA N-glycosidase
20	148	26.0	106	2	B39761	abrin (clone 3.7)
21	147.5	25.9	278	2	A39817	rRNA N-glycosidase
22	146	25.7	289	1	RL1RT	rRNA N-glycosidase
23	145	25.5	247	1	JU0393	karasurin - Mongol
24	145	25.5	289	2	JC5606	karasurin C - Tric
25	140	24.6	247	2	JC5032	karasurin-B - Tric
26	138.5	24.3	286	1	RLPUGG	beta-luffin - smoo
27	137.5	24.2	278	2	S23519	beta-luffin - smoo
28	137	24.1	286	2	S25560	rRNA N-glycosidase
29	135	23.7	528	1	TZLSA	abrin-a precursor

#### ALIGNMENTS

##### RESULT 1

S28421  
rRNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed  
N:Alternate names: antiviral protein alpha-PAP  
C:Species: Phytolacca americana (Virginian pokeweed)  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Jun-2000  
C:Accession: S28421  
R:Kataoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Kotwal, A.  
Plant Mol. Biol. 20, 879-886, 1992  
A:Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral prot  
A:Reference number: S28421; M0ID:9309240; PMID:1281438  
A:Accession: S28421  
A:Molecule type: DNA  
A:Residues: 1-294 <KAT>  
A:Cross-references: EMBL:D10600; NID:g218010; PIDN:BA01451.1; PID:g218011  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase  
F:30-278/Domain: rRNA N-glycosidase homology <RNG>

Query Match 80.3% Score 457; DB 2; Length 294;

Best Local Similarity 82.68; Pred. No. 6.9e-38;

Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSFVKTEAFPLVAIQVSEAFKTYENOVKNFNRAPFDPKVINLEEKMKISE 61

DB 177 GVDSFVKTEAFPLVAIQVSEAFKTYENOVKNFNRAPFDPKVINLEESMCKIST 236

OY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKVVNGTCQTT 110

DB 237 AIHNAKNGALTSPLLEKNGSKWIVLRVDDIEPDVGLKVVNGTCQAT 285

##### RESULT 2

S17757  
rRNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed  
N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-  
C:Species: Phytolacca americana (Virginian pokeweed)  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Aug-1999  
C:Accession: S17757; S02792; S13469; S32611  
R:Lin, O.; Chen, Z.C.; Antoniw, J.F.; White, R.F.  
Plant Mol. Biol. 17, 609-614, 1991  
A:Title: Isolation and characterization of a cDNA clone encoding the anti-viral prote  
A:Reference number: S17757; M0ID:92003676; PMID:1912488  
A:Accession: S17757  
A:Molecule type: DNA  
A:Residues: 1-313 <LIN>  
A:Cross-references: EMBL:X5383; NID:g20421; PIDN:CAA39054.1; PID:g20422  
R:Barbieri, L.; Bolognesi, A.; Genini, P.; Falasca, A.I.; Minghetti, A.; Garofano, L.  
Biochem. J. 257, 801-807, 1989  
A:Title: Ribosome-inactivating proteins from plant cells in culture.  
A:Reference number: S02792; M0ID:89193489; PMID:2930487  
A:Accession: S02792

A: Molecule type: protein  
A: Residues: 23-55, 'X', 57-65 <BAR>  
R: Biologues: A., Barbieri, L., Abbondanze, A.; Falasca, A.I.; Canticelli, D.; Battelli, R. *Biophys. Acta* 1087, 293-302, 1990  
A: Title: Purification and properties of new ribosome-inactivating proteins with RNA N-glycosidase activity  
A: Reference number: S13469; MUID:91064383; PMID:2248976  
A: Accession: S13469  
A: Molecule type: protein  
A: Residues: 23-54 <BOL>  
R: Biorn, M.J.; Larrick, J.; Platak, M.; Wilson, K.J. *Biophys. Acta* 790, 154-163, 1984  
A: Title: Characterization of translational inhibitors from *Phytolacca americana*. Amino-t  
A: Reference number: S32610; MUID:85023392; PMID:6091760  
A: Accession: S32611  
A: Molecule type: protein  
A: Residues: 23-54 <BUO>  
C: Superfamily: RNA N-glycosidase: rRNA N-glycosidase homology  
C: Keywords: glycosidase; hydrolase  
F: 1-72/Domain: signal sequence #status predicted <IG>  
F: 23-311/Product: rRNA N-glycosidase PAP #status experimental <MAT>  
F: 28-277/Domain: rRNA N-glycosidase homology <RNG>

Query Match	79.8%	Score 454	DB 2	Length 313
Best Local Similarity	82.6%	Pred. No. 1.5e-37		
Matches 90	Conservative	5	Mismatches 14	Indels 0
			Gaps	0

**DQ** 2 GVDSFPRKTEAFLVLAIQWYSEARFKYLINQVKTNFNRAEFPDPKYINLEEKWKGIS E 61  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
**Dd** 176 GVMSTFEKTEAEFLVAIQWYSEARFKYLINQVKTNFNRAFPNPKNVLQDETGWKIST 239

QY 62 AHNKNGALPKPLELDVDAKGTWYLVRVDEINRDVALIKYVNGTCQT 110  
 |||:||||| ||||| ||||| ||||| |||:|||||  
 Db 236 AHDKNGVLPKPLELDVDSGAKWYLVRVDEIKPDVALINYYVGGSCQT 284

### RESULT 3

antiviral protein - Virginian pokeweed  
C:Species: *Phytolacca americana* (Virginian pokeweed)  
C:Date: 12-Mar-1993 #sequence-revision 12-Mar-1993 #text-change 07-May-1999

R:Kung, S.S.; Kimura, M.; Funatsu, G.  
Agric. Biol. Chem. 54, 3301-3318, 1990

A:Accession: JF0401  
 A:Title: The complete amino acid sequence of antiviral protein from the seeds of pokeweed  
 A:Reference number: JF0401; NCID:91242096; PMID:1366643

A;Molecule type: protein  
A;Residues: 1-261 <KUN>

A; Experimental source: seed

C:Comment: This protein prevents the replication of a number of plant viruses, and inhibits the replication of the tobacco etch virus.  
C:Superfamily: RNA N-glycosylase: RNA N-glycosylase homology  
C:Keywords: disulfide bond; glycoprotein  
F:6-254/Domain: RNA N-glycosylase homology <RNC>  
F:10-44,245/Binding site: carboxylate (asn) (covalent) #status experimental  
F:34-250,84-105/Disulfide bonds: #status experimental

Query Match	75.48;	Score 429;	DB 2;	Length 261;
...	...	...	...	...

Best Local Similarity	78.9%	Pred. NO. 3,6e-35;
Matches	86;	Conservative
	5;	Mismatches
	18;	Indels
	0;	Gaps
	0	

Dy 2GVDSFPAKTEAFELFLVAIQMVSEARFKYLLENQVKNFNRAEFPDPXVINLEEKWKISE.61  
| | | | | | | | | | | | | | : | | | | |  
Db 153 GGGSTFEKIEAKFLVIAIQMVSEARFKYLENQVKNFNRDPSNDKVLDEENWKGIST 212

```

QY      562 AIHNAKNGALPRLELVDAKGTWYLVRADEINRDVALLKYVNGTCQTT 1100
      |||:|||||||:| ||||| ||| ||| |||||
DB      213 AIHNSKNGALPRLELVDAKGTWYLVRADEIKPDVGLLYVNGTCQAT 2611

```

RESULT 4  
JC4811  
betavulgin - beet  
C;Species: Beta vulgaris (beet)

C:\Date: 15-Aug-1996 #sequence\_revision 15-Oct-1996 #text\_change 20-Jun-2000  
C:\Accession: TC4811

A:Reference number: J04811; MUID:96235141; PMID:8666251

A: Accession: C4811  
A: Molecule type: mRNA  
A: Residues: 1-272 <OR>  
A: Cross-references: EMBL:X85567; NID:q1405840; PID:CA959952.1; PID:q1405843  
A: Note: the source is designated as *Beta vulgaris vulgaris* (mangold)  
C: Comment: This protein belongs to ribosome-inactivating protein type II.  
C: Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C: Superfamily: rRNA N-glycosidase homology <RNG>  
C: 28-271/Domain: rRNA N-glycosidase homology

Query Match	37.8%	Score 215;	DB 2;	Length 272;
Best Local Similarity	48.0%	Pred. No. 6.9e-14;		
Matches 48;	Conservative 14;	Mismatches 34;	Indels 4;	Gaps 1;

```
QY      4 DSFFVKTEAEFLLVAIQMVSEARFRFYIENOVKTNFNRAPFDPPKVINLLEEKMGKISAI 63
        | | :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     176 DSDYRSEARFLLAIQMVAEAREFYVESKAINN---VVPDYKVPSELNNNSKISGI 211
```

```
QY      64  HNAKNGALPKPLEVDAKGTKIVLRVDEINRDVALLKYY 103
          | : : : : | | : : : | : : : |
Db      232  RKAVKKVISPPIELVNASNGKMTVNQVSDIKPDMGILSYV 271
```

## RESULT 5

rRNA N-glycosylase (EC 3.2.2.22) precursor - *Gelonium multiflorum*  
N:Alternate names: gelonin, type I ribosome-inactivating protein  
C:Species: *Gelonium multiflorum*  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Aug-1999

R; Nolan, P.A.; Garrison, D.A.; Better, M

A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein  
A:Reference number: JT0753; MUID:94085781; PMID:7916721

A;Accession: JT0753

A: Molecule type: mRNA  
A: Residues: 1-316 <NOI

R. Resnades, L. Laroche, N. D. Lappi, D. A. Cross: references: GB:112243; NID:9388633; PIDN:AAA16312.1; PID:9388634  
R. Monteucchi, P. C. Lazzerini, A. M. Barberis, L. Slipe, F. Soria, M. Lappi, D. J. Rept. Protein Res. 33, 263-267, 1989

A:Title: Nterminal sequence of some ribosome-inactivating proteins  
A:Reference number: S16331; MUID:89326691; PMID:2753596

A:Accession: S16489  
A:molecule type: protein

A;Residues: 47-89, 'K', 91-92, 'D' <MON>

C;Function:

A:Description: hydrolyzes the N-glycosidic bond of a specific  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C/keywords: glycosidase; hydrolase  
F:1-46/Domain: signal sequence #status predicted <SIG>

F:47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>  
E:53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 37.5%; Score 213.5; DB 2; Length 316

Matches	47; Conservative	20; Mismatches	41; Indels	1; Gaps	1;
Qy	3	VDSFPVKTEAFLLVAIQMVSEARFKYIENQYKTNFNRAFYPPDKVINLEKKKCKISEA	62		

Dd 191 IDNYKPTFIASSLVVIQWVSEAAFTFIENQIRNNFQQRIPANNITISLENKKGKLSFQ 250

Oy 63 IH-NAKNCALPKPLELDVAKGTWIVLRVDEINRDVALLKTVNGTCOTT 110

```
Db      251 IRTSGANGMFSEAVELERANGKKYYTAVDQVKPKIALILKFVDKDPKTS 299
```

RESULT  
S46239

```

Ribosome-inactivating proteins - Virginian pokeweed
C:Species: Phytolacca americana (Virginian pokeweed)
C>Date: 10-Dec-1994 #sequence_revision 12-May-1995 #text_change 28-May-1999
C:Accession: 546239
R:Poyet, J.L.; Radom, J.; Hoeveler, A.
A:Title: Isolation and characterization of a cDNA clone encoding the pokeweed antiviral
A:Reference number: 546239; MUID:94307398; PMID:8034016
A:Accession: 546239
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-310 <POY>
A:Cross-references: GB:78628; NID:9517180; PID:CAA5342.1; PID:9517181
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F:29-282/Domain: rRNA N-glycosidase homology <RNG>

Query Match          35.1%; Score 200; DB 2; Length 310;
Best Local Similarity 43.5%; Pred. No. 2,5e-12;
Matches 47; Conservative 20; Mismatches 29; Indels 12; Gaps 5;

Oy 9 KTEAFELLVAIOWSEARFKYIENOVKTNPNR--FYDPKYNLEEKKGKISEAIHNA 66
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 KNEAEFLLIWQWTEASRFKYIENKAKFEDDANGYQPPKALISLEKMNDSVSKI--A 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 67 KNG-----ALPKPELVDAKGTKWIYLRVDEINRDV--ALLKYVCTGO 108
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 KVGTSGDSTVTLPGDLKDENNKPTWTATYMDLKDINDIALTLHV--TK 285
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
RLCSAG
agglutinin precursor - castor bean
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: A24261; A24210
R:Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J: Biol. Chem. 260, 15682-15686, 1985
A:Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A:Reference number: A24261; MUID:86059449; PMID:2999130
A:Accession: A24261
A:Molecule type: mRNA
A:Residues: 1-564 <ROB>
A:Cross-references: GB:M12089; NID:q169700; PID:AAA33869.1; PID:q169701
R:Maeki, T.; Yoshioke, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A:Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
A:Reference number: A24210
A:Accession: A24210
A:Molecule type: protein
A:Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-564
C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; see:
F:1-124/Domain: signal sequence #status predicted <SIG>
F:32-320/Product: agglutinin chain A #status predicted <ACH>
F:33-281/Domain: rRNA N-glycosidase homology <RNG>
F:303-564/Product: agglutinin chain B #status experimental <BCH>
F:319-361,362-402,403-443,450-485,489-528,531-564/Region: 40-residue repeats
F:34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:200,403/Active site: Glu, Arg #status predicted
F:282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F:324,337,348/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status predicted
F:337,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

```

Db 184 IPTLANSFWMC10MISMAAREFYIEGEMRRIRINRNSAPDPVITLSEWGNLSTALQ 243

Oy 66 AKNGALPKLELVDAKGTWIVLRVDEINRDVALKY 102

Db 244 SNOGAFASPIQLOLRNRSKFNVDVSLIPIALMY 280

RESULT 8

RUCSD

ricin D precursor - castor bean

C:Species: Ricinus communis (castor bean)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

C:Halling, K.C.; Halling, A.C.; Murray, E.E.; Tadin, B.F.; Houston, L.L.; Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A:Reference number: A24041; MUID:86067214; PMID:2999712

A:Accession: A24041

A:Molecule type: DNA

A:Residues: 1-576 <HAL>

A:Cross-references: GB:003179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R:Tregear, J.W.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A:Reference number: S20513; MUID:92163016; PMID:1371405

A:Accession: S20513

A:Molecule type: DNA

A:Residues: 1-576 <TRE>

A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA7095.1; PID:g21085

R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 265-270, 1985

A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.

A:Reference number: A24614; MUID:85179479; PMID:3838723

A:Accession: A24614

A:Molecule type: mRNA

A:Residues: 15-75, 'D', '77-550, 'R', '552-576 <LAM>

A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26330.1; PID:g21078

R:Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A:Title: Isolation and sequences of peptic peptides, and the complete sequence of the

A:Reference number: A03372

A:Accession: A03372

A:Molecule type: Protein

A:Residues: 36-97, 'Q', '99-109, 'S', '111-269, 'D', '272-283, 'L', '285-288, 290-302 <YOS>

A:Note: this paper cites the others in the series providing experimental details for

R:Ataki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptop

A:Reference number: A24010

A:Accession: A24010

A:Molecule type: Protein

A:Residues: 315-383, 'PS', '386-576 <ARA>

R:Funatsu, G.; Kimura, M.; Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A:Title: Primary structure of Ala chain of ricin D.

A:Reference number: A03374

A:Accession: A03374

A:Molecule type: Protein

A:Residues: 315-335, 'N', '337-342, 'NH', '345-362, 364-383, 'PS', '386-399, 'T', '401, 'D', '403, 'E', '527, 'E', '529-564, 'W', '566, 'H', '567-570, 'LI', '573-574, 'F' <FUN>

A:Note: this paper, one of a series, summarizes the experimental details for the dete

R:Ready, M.P.; Kim, Y.; Roberts, J.D.

Proteins 10, 270-278, 1991

A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanis

A:Reference number: A48237; MUID:91352006; PMID:1861863

R:Rutenber, E.; Roberts, J.D.

Proteins 10, 260-269, 1991

A:Title: Structure of ricin B-chain at 2.5 angstrom resolution.

A:Reference number: A48238; MUID:91352005; PMID:1861862

A:Contents: annotation; X-ray crystallography, 2.5 angstroms

R:Katzin, B.J.; Collins, E.J.; Roberts, J.D.

Proteins 10, 251-259, 1991  
 A:Title: Structure of ricin A-chain at 2.5 angstroms.  
 A:Reference number: A48239; MUID:91352004; PMID:1881881  
 A:Contents: annotation: X-ray crystallography, 2.5 angstroms  
 C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which into the cell of the A chain inhibits protein synthesis. It inactivates the 60S ribosomal subunit.  
 C:Comment: This protein is cytotoxic and very poisonous to animals.  
 C:Superfamily: ricin; RNA N-glycosidase homology  
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
 F:1-35/Domain: signal sequence #status predicted <SIG>  
 F:35-302/Product: ricin D chain A #status experimental <ACH>  
 F:46-293/Domain: RNA N-glycosidase homology <RNG>  
 F:313-373/Product: ricin D chain B #status experimental <BCH>  
 F:331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats  
 F:45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:115,156,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F:212/Active site: Glu #status experimental  
 F:215/Active site: Arg #status predicted  
 F:294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental  
 F:336,349,360/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental  
 F:348,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental

Query Match 33.7%; Score 192; DB 1; Length 576;  
 Best Local Similarity 39.8%; Pred. No. 3.2e-11;  
 Matches 41; Conservative 19; Mismatches 39; Indels 4; Gaps 2;

Oy 2 GVDSPVYTEAFLLVAIOWVSEARFKYIENOVKTNNRATYPPDKVINEEKWKI 59  
 Db 192 GGTOLPLTARSF--ITCIOMISEARFOYLEGERTRTYRARSAPDSVITLESWGL 249  
 Oy 60 SEAHNAKNGALPRLPLEVDAGKTWIVLRVDEINRDVALKY 102  
 Db 250 STAIQESNOGAFASPIQLQRRNGSKFSVYDSILPIALMVY 292

RESULT 9  
 S17932  
 RNA N-glycosidase (EC 3.2.2.22) Sap3 - common soapwort (fragment)  
 N:Alternate names: saporin 3  
 C:Species: Saponaria officinalis (common soapwort)  
 C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 20-Aug-1999  
 C:Accession: S17932; S15458  
 R:Fordham-Skelton, A.P.; Taylor, P.N.; Hartley, M.R.; Croy, R.R.D.  
 M:1. Gen. Genet. 229, 460-466, 1991  
 A:Title: Characterisation of saporin genes: in vitro expression and ribosome inactivation  
 A:Reference number: S17932; MUID:92049247; PMID:1719367  
 A:Accession: S17932  
 A:Molecule type: DNA  
 A:Residues: 1-236 <FOR>  
 A:Cross-references: EMBL:X59256; NID:921322; PIDN:CAA1949.1; PID:921323  
 A:Note: the authors translated the codon CTC for residue 75 as Phe and GCA for residue 1  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase; monomer; toxin  
 F:1-221/Domain: RNA N-glycosidase homology (fragment) <RNG>

Query Match 30.9%; Score 176; DB 2; Length 236;  
 Best Local Similarity 44.0%; Pred. No. 4.4e-10;  
 Matches 44; Conservative 15; Mismatches 33; Indels 8; Gaps 3;

Oy 8 VKTEAFLLVAIOWVSEARFKYIENOVKTNNRATYPPDKVINEEKWKISAIH-NA 66  
 Db 132 VKNEARFLITAIOMTAEARFRYIQLTKNPFNKENSEKVIQFVNMKISKAIYGD 191  
 Oy 67 KNGALPRLPLEVDAGKTWIVLRVDEINRDVALKYNGT 106  
 Db 192 KNGVFNKDYDFGFGK-----VRQVKDL--QMGFLMVLGTT 224

RESULT 10  
 A58923  
 RNA N-glycosidase (EC 3.2.2.22) saporin S9 - common soapwort  
 C:Species: Saponaria officinalis (common soapwort)

C:Date: 31-Dec-2001 #sequence-revision 31-Dec-2001 #text-change 01-Mar-2002  
 C:Accession: A58923  
 R:Mastrorillo, M.; Di Marco, A.; Ferranti, P.; Bolognesi, A.; Stirpe, F.; Parente, A.  
 Submitted to the Protein Sequence Database, December 1998  
 A:Description: Saporin-S9, the most basic ribosome-inactivating protein from Saponaria  
 A:Reference number: A58923  
 A:Accession: A58923  
 A:Molecule type: protein  
 A:Residues: 1-253 <MAS>  
 A:Experimental source: seeds  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase; toxin

Query Match 30.1%; Score 171.5; DB 2; Length 253;  
 Best Local Similarity 56.7%; Pred. No. 1.3e-09;  
 Matches 38; Conservative 6; Mismatches 22; Indels 1; Gaps 1;

Oy 8 VKTEAFLLVAIOWVSEARFKYIENOVKTNNRATYPPDKVINEEKWKISAIH-NA 66  
 Db 160 VKNEARFLITAIOMTAEARFRYIQLTKNPFNKENSEKVIKEVNMKISAIHIDA 219  
 Oy 67 KNGALPRL 73  
 Db 220 KNGVFNK 226

RESULT 11  
 JC4840  
 RNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd  
 C:Species: Trichosanthes anguina (snake gourd)  
 C:Date: 15-Aug-1996 #sequence-revision 24-Oct-1997 #text-change 05-Dec-1997  
 C:Accession: JC4840; JT0701; JT0677  
 R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.  
 Biomed. Sci. 3, 178-186, 1996  
 A:Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein fr  
 A:Reference number: JC4840  
 A:Accession: JC4840  
 A:Molecule type: protein  
 A:Residues: 1-132, 'S', 134-245 <CHO1>  
 A:Experimental source: seed  
 A:Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Ta  
 R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.  
 Submitted to JIPID, August 1995  
 A:Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein  
 A:Reference number: JT0677  
 A:Accession: JT0701  
 A:Molecule type: protein  
 A:Residues: 1-50, 'L', 52-245 <CHO2>  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed  
 F:4-242/Domain: RNA N-glycosidase homology <RNG>  
 F:51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:70,158,161/Active site: Tyr, Glu, Arg #status predicted  
 F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 30.0%; Score 170.5; DB 2; Length 245;  
 Best Local Similarity 38.2%; Pred. No. 1.6e-09;  
 Matches 39; Conservative 20; Mismatches 38; Indels 5; Gaps 2;

Oy \*6 FPKTEAFLLVAIOWVSEARFKYIENOVKTNNRATYPPDKVINEEKWKISAIH 65  
 Db 140 YDQSTAAALVITQSTAEARKYIEQVSSHSNFPNOAVISLENKGAISKOI 199  
 Oy 66 AK--NGALPRLPLEVDAGKTWIVLRVDE--INRDVALKY 102  
 Db 200 ANRTHGQFENPELVNPGDTRFSVHTSAGVYKKGKIKLLY 241

RESULT 12  
 RLQHG2  
 RNA N-glycosidase (EC 3.2.2.22) Sap2 precursor - common soapwort  
 N:Alternate names: ribosome-inactivating protein; saporin 2; saporin S5  
 C:Species: Saponaria officinalis (common soapwort)



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 15.912 Seconds  
(without alignments)  
1424.413 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569  
Sequence: 1 MGVSDFPKTEAFELVAIQ.....DEINRVALLKRYNGTCOTT 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mmc:\*  
9: sp\_organelle:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564	99.1	314	10	P93444
2	559	98.2	262	10	O8S946
3	449	78.9	313	10	O941G8
4	438	77.0	339	10	O8RYA4
5	429	76.8	315	10	O9XFF8
6	429	75.4	261	10	O8S947
7	355	62.4	237	10	O9ATB3
8	302	53.1	302	10	P93077
9	213	37.8	272	10	O93418
10	212.5	37.3	258	10	O9S9E4
11	207.5	36.5	279	10	O9MSK6
12	197.5	34.7	279	10	O9AUES3
13	192	33.7	541	10	O41174
14	188.5	33.1	305	10	O8M4U4
15	170.5	30.0	294	10	O93Y65
16	170.5	30.0	294	10	O93Y64

17	154.5	27.2	294	10	O93Y66	O93Y66 dianthus ch
18	149	26.2	289	10	P93261	P93261 mesembryant
19	147.5	25.9	549	10	O9FV22	O9FV22 cinanomum
20	147.5	25.9	580	10	O94BW3	O94BW3 cinanomum
21	147.5	25.9	581	10	O94BW5	O94BW5 cinanomum
22	146.5	25.7	270	10	O9S4O5	O9S4O5 amarantlus
23	146.5	25.7	319	10	O8VWY2	O8VWY2 spiracila ol
24	146	25.7	289	10	O94KE4	O94KE4 trichosanthe
25	145	25.5	247	10	O9LRE3	O9LRE3 trichosanthe
26	145	25.5	289	10	O41216	O41216 trichosanthe
27	145	25.5	382	10	O8S4A3	O8S4A3 abrus prece
28	144	25.3	270	10	O41611	O41611 trichosanthe
29	143.5	25.2	279	10	O92T25	O92T25 amarantlus
30	143.5	25.2	284	10	O96322	O96322 amarantlus
31	143.5	25.2	580	10	O94BM4	O94BM4 cinanomum
32	138	24.3	293	10	O8VYU0	O8VYU0 jatropa cu
33	137.5	24.2	251	10	O48859	O48859 amarantlus
34	137.5	24.2	278	10	O00980	O00980 luffa cylin
35	137	24.1	286	10	O9FUV7	O9FUV7 momordica c
36	135	23.7	252	10	O38761	O38761 abrus prece
37	134	23.6	565	10	O04071	O04071 sambucus nl
38	134	23.6	566	10	O04072	O04072 sambucus nl
39	133.5	23.5	604	10	O9M654	O9M654 polyonatum
40	133	23.4	293	10	O8S4S2	O8S4S2 jatropa cu
41	133	23.4	547	10	O9M6E9	O9M6E9 abrus prece
42	132.5	23.3	570	10	O22415	O22415 sambucus nl
43	132.5	23.3	603	10	O9M653	O9M653 polyonatum
44	132	23.2	264	10	O9F5H2	O9F5H2 momordica c
45	132	23.2	286	10	O41257	O41257 momordica c

## ALIGNMENTS

RESULT 1  
P93444 PRELIMINARY: PRT: 314 AA.  
ID P93444;  
AC P93444;  
DT 01-MAY-1997 (TRENBLREL 03, Created)  
DT 01-MAY-1997 (TRENBLREL 03, Last sequence update)  
DT 01-MAR-2002 (TRENBLREL 20, Last annotation update)  
DE rRNA-glycosidase precursor (EC 3.2.2.22).  
GN PAP-S.  
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).  
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SEED:  
RX MEDLINE=97263479; PubMed=9109394;  
RA Poyet J.L., Hoeveler A.:  
RT "CDNA cloning of the gene encoding the Antiviral Protein from the  
RT seeds of Phytolacca americana and its expression in E.coli.";  
RL FEBS Lett. 406:97-100(1997).  
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
CC EMBL: X98079; CA66702.1; -;  
DR HSSP: Q03464; IAPA.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP. 1.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA\_RICIN. 1.  
KW Hydroxylase; Signal; Toxin.  
FT SIGNAL 1 24  
FT CHAIN 25 314 POTENTIAL.  
SQ SEQUENCE 314 AA; 35323 MW; A89E3CE57789F9E CRC64;  
Query Match 99.1%; Score 564; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 3e-52;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Caps 0;



QY	2	GVDSFPVKTAEFFLLVAIOMSEARFKYIENQVKNFNRAFPDPKVINLEEKWKIS	61
Db	178	GVDSFPVKTAEFFLLVAIOMSEARFKYIENQVKNFNRAFPDPKVINLEEKWKIS	237
QY	62	AHHAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKVNGTCQT	110
Db	238	AHHAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKVNGTCQT	286
RESULT 2			
ID	08S946	PRELIMINARY:	PRT: 262 AA.
AC	08S946:		
DT	01-JUN-2002	(TREMBLrel. 21, Created)	
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	PAP-S2 (Fragment).		
GN	PAP-S2.		
OS	Phytolacca americana (Common pokeweed) (Virginian pokeweed).		
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:		
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:		
OC	Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.		
OX	NCBI_Taxid=3527;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RA	Honjo E., Watanabe K.:		
RT	"Cloning of genomic DNA encoding two types of pokeweed antiviral		
RT	protein in seeds, PAP-S1 and PAP-S2, and functional comparison of		
RT	their recombinant proteins with other PAP isoforms."		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB071855; BAB86350.1; --		
FT	NON_TER	1	262
FT	NON_TER	262	1
SO	SEQUENCE	262 AA;	29486 MW; AF2D010A73C9D18B CRC64;
Query Match			
		98.2%;	Score 559; DB 10; Length 262;
		Best Local Similarity	99.1%; Pred. No. 8,3e-52;
	Matches 108;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0
QY	2	GVDSFPVKTAEFFLLVAIOMSEARFKYIENQVKNFNRAFPDPKVINLEEKWKIS	61
Db	154	GVDSFPVKTAEFFLLVAIOMSEARFKYIENQVKNFNRAFPDPKVINLEEKWKIS	213
QY	62	AHHAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKVNGTCQT	110
Db	214	AHHAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKVNGTCQT	262
RESULT 3			
ID	0941G8	PRELIMINARY:	PRT: 313 AA.
AC	0941G8:		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)	
DE	rRNA - glycosidase (EC 3.2.2.22).		
GN	PAP.		
OS	Phytolacca acinosa.		
OC	Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;		
OC	Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.		
OX	NCBI_Taxid=107615;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RA	Peng X., Yuan J., Qiang B.:		
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE		
CC	SPECIFIC ADENOSINE ON THE 265 RNA.		
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.		
DR	EMBL; AY049785; AAL15442.1; --		
DR	Interpro: IPR001574; RIP.		
DR	Pfam: PF00161; RIP; 1.		

Query Match	78.9%	Score 449	DB 10	Length 313
Best Local Similarity	81.7%	Pred. No. 6,3e-40		
Matches 89	Conservative 5	Mismatches 15	Indels 0	Gaps 0

  

QY	2	GVDSFPVTEAFPLLVAIOMVSEARFVYIEQVKTNNRAFPDPKYNLEKNGKISKE	61
DB	176	GVSTSTETETAEFLVLAIVOMVSEARFVYIQGVKTNNRAFPDPKYNLEETGKIST	235

  

QY	62	AIHAANKALPKPELVDAKSTKIVLEVDENRPAVLTKVNCQOTT	110
DB	236	AIHAANKNVLPKPELVDAKSAKIVLEVDLKPVALLNLYGSCOTT	284

  

RESULT 4	ID	08RYA4	PRELIMINARY:	PRT:	339 AA.
AC	08RYA4				
DT	01-JUN-2002	(TREMBLrel. 21, Created)			
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)			
DE		Ribosome inactivating protein type 1 precursor.			
OS		Phytolacca americana (Common pokeweed)			
OC		Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;			
OC		Spermatophyta, Magnoliophyta: eudicotyledons: core eudicots;			
OC		Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.			
OX		NCBI_TaxID=3527;			
XX		[1]			
XX		SEQUENCE FROM N.A.			
RA		Park S.-W., Lawrence C.B., Linden J.C., Vivanco J.M.;			
RT		"Characterization of a novel ethylene-inducible ribosome-inactivating			
RT		protein exuded from root cultures of Phytolacca americana."			
RL		Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.			
DR		EMBL: AY071928; AAL61546.1; -			
KW		Signal.			
FT		SIGNAL.			
QO	SEQUENCE	339 AA: 37978 MW: 7047BDC2EDDD965F CRC64:			
		1 47 POTENTIAL.			

	Query Match	77.0%	Score 438	DB 10	Length 339
	Best Local Similarity	80.4%	Pred. No. 1,1e-38		
	Matches	86	Conservative	4	Mismatches 17; Indels 0; Gaps 0
QY	2	GVDSPFYKTEAFELFLVLAIDWSEARFXYIENQVNTNENRFAEPDPKVINLEEKMGKISE	61		
Db	203	GVSSEFEKTEAEGLFLVLAIDWSEARFXYIENQVNTNENRFAEPDPKVINLEEKMGKISE	262		
QY	62	AHNANKGALPKPLELVDAQKGTWVLVVDENRVALTKVTNCTQ	108		
Db	263	AHGANKGAFSKPLELVDAQGNKMWLVRYDEIKSDVGLTKVTGSCQ	309		
RESULT 5					
	09XFF8				
ID	09XFF8	PRELIMINARY:	PRT:	315 AA.	
AC	09XFF8:				
DT	01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DE	1-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DT	rRNA - glycosidase (EC 3.2.2.22).				
GN	PIP2.				
OS	Phytolacca insularis				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Caryophyllales; Caryophyllaceae; Phytolacca.				
OX	NCBI_TaxID=63744:				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=20505377; PubMed=11052196;				
RT	Song S.K., Choi Y., Moon Y.H., Kim S.G., Choi Y.D., Lee J.S.;				
RT	"Systemic induction of a Phytolacca insularis antiviral protein gene				
RT	by mechanical wounding, jasmonic acid, and abscisic acid";				
RT	by mechanical wounding, jasmonic acid, and abscisic acid";				

```

RL Plant Mol. Biol. 43:439-450(2000).
CC -i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF141331: AAD32679.1: -.
DR HSSP: 003464: IAPA.
DR InterPro: IPR001574: RIP.
DR Pfam: PF00161: RIP; 1.
DR PRINTS: PR00396: SHIGARICIN.
DR PROSITE: PS00275: SHIGA_RICIN; UNKNOWN_1.
KM Hydrolase: Toxin.
SQ SEQUENCE 315 AA: 35728 MW: F85DE21154B5FA15 CRC64:

Query Match
Best Local Similarity 76.8%; Score 437; DB 10; Length 315;
Matches 86; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 2 GVDSPVTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPPKYINLEEKKGKISE 61
DB 179 GVDITNTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPAKYINLEETGKIST 238
62 AIHNAKNGALPKPLVDPAKGTKWIVLRVDEINRDVALTKYNGTCQTT 110
239 AIHDAKNGALTKPLDLINEDGTKWIVLRVDEIKPVGLLNYDGTGCTT 287

RESULT 6
QY 08S947 PRELIMINARY: PRT: 261 AA.
DB 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE PAP-S1 (Fragment).
GN PAP-S1.
OS Physiolacca americana (Common pokeberry) (Virginian pokeweed);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Honjo E., Watanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBD databases.
DR EMBL: AB071854; BAB86349.1: -.
FT NON_TER 1 1
FT NON_TER 261 261
SQ SEQUENCE 261 AA: 29199 MW: D88B998BFEF1F989 CRC64:

Query Match
Best Local Similarity 75.4%; Score 429; DB 10; Length 261;
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPVTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPPKYINLEEKKGKISE 61
DB 153 GCGSTETKEAFELVAIOMVSEARFYIENOVNTNFRAPYPPDKYIDLEENNGKIST 212
62 AIHNAKNGALPKPLVDPAKGTKWIVLRVDEINRDVALTKYNGTCQTT 110
213 AIHNAKNGALPKPLVDPAKGTKWIVLRVDEIKPVGLLNYNGTCQAT 261

RESULT 7
QY 09ATB3 PRELIMINARY: PRT: 237 AA.
DB 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
RNA -91ycosidase (EC 3.2.2.22) (Fragment).

```

```

GN MPAP.
OS Physiolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen D., Wang X., Zhou G.;
RT "Pokeweed antiviral protein gene, partial cds.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBD databases.
CC -i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF38910: AAK21951.1: -.
DR HSSP: P10297: IOCG.
DR InterPro: IPR001574: RIP.
DR Pfam: PF00161: RIP; 1.
DR PRINTS: PR00396: SHIGARICIN.
DR PROSITE: PS00275: SHIGA_RICIN; 1.
KM Hydrolase: Toxin.
FT NON_TER 1 1
FT NON_TER 237 237
SQ SEQUENCE 237 AA: 26534 MW: FE4ADCEB03464783 CRC64:

Query Match
Best Local Similarity 62.4%; Score 355; DB 10; Length 237;
Matches 70; Conservative 83.3%; Pred. No. 5.3e-30;
Matches 70; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 GVDSPVTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPPKYINLEEKKGKISE 61
DB 154 GVMSTETKEAFELVAIOMVSEARFYIENOVNTNFRAPYPPKYLNETGKIST 213
62 AIHNAKNGALPKPLVDPAKGTKW 85
214 AIHAKNGVLPKPLVDPAKSGAKW 237

RESULT 8
QY 093077 PRELIMINARY: PRT: 302 AA.
DB 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE RNA -91ycosidase (EC 3.2.2.22).
GN RIP.
OS Clerodendrum aculeatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Clerodendrum.
OX NCBI_TaxID=54208;
RN [1]
RP SEQUENCE FROM N.A.
RA Kumar D., Verma H.N., Tuleja N., Tewari K.K.;
RT "Cloning and characterization of a gene encoding an antiviral protein
RT from Clerodendrum aculeatum L.";
RL Plant Mol. Biol. 33:745-751(1997).
CC -i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: X96474: CA65328.1: -.
DR EMBL: X96583: CA65402.1: -.
DR HSSP: P10297: IOCG.
DR InterPro: IPR001574: RIP.
DR Pfam: PF00161: RIP; 1.
DR PRINTS: PR00396: SHIGARICIN.
DR PROSITE: PS00275: SHIGA_RICIN; 1.
KM Glycosidase; Hydrolase; Toxin.
SQ SEQUENCE 302 AA: 33955 MW: B0561C3918C2E6A2 CRC64:

```

Query Match 53.1%; Score 302; DB 10; Length 302;  
 Best Local Similarity 58.9%; Pred. No. 3.4e-24;  
 Matches 63; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

OY 2 GVDSFVKTAEFFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISE 61  
 DB 176 GYRAETKEVEAFFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKIST 235  
 OY 62 AHNKNGALPKLELVDAKGTWIVLRDEINRDVALIKYNGTCQ 108  
 DB 236 PIRNANGVISPPLNINSGEDPMWTVRVDEIKPIYALLNFGSGTCQ 282

## RESULT 9

OY 039418 PRELIMINARY: PRT: 272 AA.  
 AC 039418;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Antiviral protein precursor (Ribosome-inactivating protein) (RNA N-glycosidase) (Polynucleotide:adenosine glycosidase) (EC 3.2.2.22)  
 DE (BETAVOLGIN) (BVG).  
 GN RIP OR BETAVOLGIN OR BVG.  
 OS Beta vulgaris (Sugar beet).  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots: Caryophyllales: Caryophyllales: Chenopodiaceae: Beta.  
 OC NCBI\_TaxID=3555;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=SEEDLING;  
 RX MEDLINE=96235141; Pubmed=8666251;  
 RA Horning E., Majumdar H., Jeske H., Mundry K.-W.;  
 RT "Cloning of a cDNA encoding a new ribosome-inactivating protein from Beta vulgaris vulgaris (mangold).";  
 RL Gene 170:233-236(1996).  
 CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN SYNTHESIS IN VITRO. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR SUICIDE UPON INVASION BY A VIRUS.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO TYPE 1 RIP.  
 CC EMBL: X85967; CA55952.1;  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP. 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; FALSE\_NEG.  
 KW Hydrolyase; Glycosidase; Antiviral; Protein synthesis inhibitor; Toxin;  
 KW Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 272 BY SIMILARITY.  
 FT ACT\_SITE 196 196 BY SIMILARITY.  
 FT SEQUENCE 272 AA: 30168 MW: 77DD0917FD12FDFR CRC64;

Query Match 37.8%; Score 215; DB 10; Length 272;  
 Best Local Similarity 48.0%; Pred. No. 6.2e-15;  
 Matches 48; Conservative 14; Mismatches 34; Indels 4; Gaps 1;

OY 4 DSFVKTAEFFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISEAI 63  
 DB 176 DSDYRSEARFAEFLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISGCI 231  
 OY 64 HNAKNGALPKLELVDAKGTWIVLRDEINRDVALIKYV 103  
 DB 232 KRAVKVISPPLNINSGEDPMWTVRVDEIKPIYALLNFGSGTCQ 271

## RESULT 10

OY 09S9E4 PRELIMINARY: PRT: 258 AA.  
 AC 09S9E4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22).  
 OS Geleonium multiflorum (Euphorbiaceae himalaya).  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots: Rosidae; eurosids I: Malpighiales; Euphorbiaceae: Geleonium.  
 OC NCBI\_TaxID=3979;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=96006751; Pubmed=7553224;  
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,  
 RA Toman P.D., Cheung L.;  
 RT "Amino acid sequence analysis, gene construction, cloning, and expression of geleonium, a toxin derived from Geleonium multiflorum.";  
 RL J. Interferon Cytokine Res. 15:547-555(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR HSSP: P09989; IMRI.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP. 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 KW Hydrolyase; Toxin;  
 SO SEQUENCE 258 AA: 28826 MW: 13D68E673F4D6B06 CRC64;

Query Match 37.3%; Score 212.5; DB 10; Length 258;  
 Best Local Similarity 44.7%; Pred. No. 1.1e-14;  
 Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

OY 3 VDSFVKTAEFFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISEA 62  
 DB 152 IDNKRPTIASLLVIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISFQ 211  
 OY 63 IH-NAKNGALPKLELVDAKGTWIVLRDEINRDVALIKYV 104  
 DB 212 IRTSGANGMFEAEVLERANGKRYVAVDQVKPKIKALKRVD 254

## RESULT 11

OY 09M5K6 PRELIMINARY: PRT: 279 AA.  
 AC 09M5K6;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22).  
 GN CAP30A.  
 OS Chenopodium album (Lamb's-quarters).  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots: Caryophyllales: Caryophyllales: Chenopodiaceae: Chenopodium.  
 OC NCBI\_TaxID=3559;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Park J.S., Cho K.J., Lee S.M., Kim Y.T., Hwang Y.S.;  
 RT "A cDNA clone encoding a novel ribosome inactivating protein from Chenopodium album L.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC EMBL: AF228508; AAF6234.1;  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP. 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 KW Hydrolyase; Toxin.  
 SO SEQUENCE 279 AA: 31377 MW: 2A5330E445DC952 CRC64;



Db 239 TTINPALQLISPSNDEWVNVKVSQISPDGILKF 272

## RESULT 15

Q93Y65 PRELIMINARY; PRT; 294 AA.  
AC Q93Y65;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE rRNA -glycosidase (EC 3.2.2.22).  
OS Dianthus chinensis.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.  
OX NCBI\_TaxID=118431;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20306826; Pubmed=10850653;  
RA Cho H.J., Lee S.J., Kim S., Kim B.D.;  
RT Isolation and characterization of cDNAs encoding ribosome  
RT inactivating protein from Dianthus sinensis L.;  
RL Mol. Cells 10:135-141(2000).  
CC -|- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
DR EMBL: AF219237; AAK68928.1; -  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.1.  
KW Hydrolase; Toxin.  
SQ SEQUENCE 294 AA; 3331 MW; 659E72DD847A72D0 CRC64;

Query Match 30.0%; Score 170.5; DB 10; Length 294;  
Best Local Similarity 55.2%; Pred. No. 4e-10;  
Matches 37; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 8 VKTEAFFLLVAIQMVSEARFYIENOVKTNFRAPYDDPKVYNLEEKWKISEAITH-NA 66  
DB 185 VKDEARFLIGIQMSAEAVFRITQNLVTRNFPKKNSDNTVIQYOTSMGKISEAITHDC 244  
QY 67 KNGCALPK 73  
DB 245 KNGKFNK 251

Search completed: July 2, 2003, 11:42:10  
Job time : 15.912 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 38.044 Seconds  
(without alignments)  
1424.413 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357  
Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALIKYVNGTCQTT 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeophages:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	1352	99.6	314	10	P93444
2	1332	98.2	262	10	O8S946
3	1099.5	81.0	261	10	O8S947
4	1044	72.0	313	10	O941G8
5	977.5	72.0	315	10	O9XFF8
6	965	71.1	339	10	O8RYA4
7	953	70.2	237	10	O8RYA4
8	701	51.7	302	10	P93077
9	425.5	31.4	289	10	P93261
10	395	29.1	279	10	O9MSK6
11	394	29.0	272	10	O39418
12	382	28.2	279	10	O9AUE3
13	368	24.2	294	10	O93Y65
14	328	24.2	294	10	O93Y65
15	321.5	23.7	258	10	O9S9E4
16	315	23.2	294	10	O93Y66

17	301	22.2	305	10	O8W404	O8W404 bougainvill
18	292	21.5	541	10	O41174	O41174 ricinus com
19	287	21.1	319	10	O8W402	O8W402 spinacia ol
20	258.5	19.0	279	10	O92725	O92725 amarantus
21	248.5	18.3	251	10	O48859	O48859 amarantus
22	243	17.9	278	10	O00980	O00980 luffa cylind
23	242	17.8	289	10	O94KE4	O94KE4 trichosanthe
24	241	17.8	247	10	O9LRE3	O9LRE3 trichosanthe
25	239	17.6	270	10	O41611	O41611 trichosanthe
26	237	17.5	270	10	O9SA05	O9SA05 amarantus
27	236	17.4	280	10	O94BW3	O94BW3 cinamomum
28	235	17.3	289	10	O41216	O41216 trichosanthe
29	234	17.2	284	10	O96322	O96322 amarantus
30	234	17.2	281	10	O94BW5	O94BW5 cinamomum
31	234	17.2	604	10	O9M654	O9M654 polygonatum
32	233.5	17.2	553	10	O94552	O94552 sambucus ni
33	231.5	17.1	566	10	O04072	O04072 sambucus ni
34	231	17.0	580	10	O94BW4	O94BW4 cinamomum
35	230.5	17.0	252	10	O38761	O38761 abrus prece
36	228	16.8	549	10	O9FV22	O9FV22 cinamomum
37	226.5	16.7	547	10	O9M6E9	O9M6E9 abrus prece
38	226	16.7	565	10	O04071	O04071 sambucus ni
39	224.5	16.5	251	10	O96236	O96236 abrus prece
40	223.5	16.5	251	10	O96237	O96237 abrus prece
41	221.5	16.3	573	10	O8W2E8	O8W2E8 iris hollan
42	219.5	16.2	592	10	O8W2E7	O8W2E7 iris hollan
43	217.5	16.0	251	10	O96235	O96235 abrus prece
44	217.5	16.0	252	10	O38760	O38760 abrus prece
45	216.5	16.0	603	10	O9M653	O9M653 polygonatum

## ALIGNMENTS

RESULT 1  
P93444 PRELIMINARY: PRT: 314 AA.  
ID P93444;  
AC P93444;  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE rRNA - glycosidase precursor (EC 3.2.2.22).  
GN PAP-S.  
OS Phytoacta americana (Common pokeweed) (Virginia pokeweed).  
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
OC Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SEED.  
RX MEDLINE=97263479; PubMed=9109394;  
RA Poyet J.L., Hoeveler A.;  
RT "CDNA cloning of the gene encoding the Antiviral Protein from the  
RT seeds of Phytolacca americana and its expression in E.coli.";  
RL FBS Lett. 406:97-100(1997).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
CC EMBL: X98079; CA66702.1; -;  
CC DR HSSP: 003464; IAPA.  
CC DR InterPro: IPR001574; RIP.  
CC DR Pfam: PF00161; RIP; 1.  
CC DR PRINTS: PR00396; SHIGARICIN.  
CC DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
CC KW Hydrolyase; Signal; Toxin.  
CC FT SIGNAL 1 24 POTENTIAL.  
CC FT CHAIN 25 314 POTENTIAL.  
CC SQ SEQUENCE 314 AA: 35323 MW: A8963CE57789FF9E CRC64;  
Query Match 99.6%; Score 1352; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 3.2e-105;  
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 INTITPDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVLOGANLK 61  
 DB 25 INTITPDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVLOGANLK 84  
 QY 62 TITLMLRRNNLYMGVSDPENGKCRHIFNDITSTERTVENTLCCSSSSRYAAMSINYN 121  
 DB 85 TITLMLRRNNLYMGVSDPENGKCRHIFNDITSTERTVENTLCCSSSSRYAAMSINYN 144  
 QY 122 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDFPKTEAFLLVAIQWSEARF 181  
 DB 145 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDFPKTEAFLLVAIQWSEARF 204  
 QY 182 KYIENQVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIYL 241  
 DB 205 KYIENQVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIYL 264  
 QY 242 RVDEINRDVALLKYVNGTCOTT 263  
 DB 265 RVDEINRDVALLKYVNGTCOTT 286

## RESULT 2

QY 08S946 PRELIMINARY: PRT: 262 AA.  
 ID 08S946  
 AC 08S946:  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE PAP-S2 (Fragment).  
 GN PAP-S2.  
 OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
 NC NCBL\_TaxID=3527;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP Honjo E., Matanabe K.:  
 RT "Cloning of genomic DNA encoding two types of pokeweed antiviral  
 RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of  
 RT their recombinant proteins with other PAP isoforms."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB071855; BAB86350.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 262 262  
 SO SEQUENCE 262 AA; 29486 MW; AF2D010X/3C9D18B CRC64;

Query Match 98.2%; Score 1332; DB 10; Length 262;  
 Best local Similarity 98.1%; Pred. No. 1.2e-103;  
 Matches 257; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 INTITPDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVLOGANLK 61  
 DB 1 INTITPDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVLOGANLK 60  
 QY 62 TITLMLRRNNLYMGVSDPENGKCRHIFNDITSTERTVENTLCCSSSSRYAAMSINYN 121  
 DB 61 TITLMLRRNNLYMGVSDPENGKCRHIFNDITSTERTVENTLCCSSSSRYAAMSINYN 120  
 QY 122 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDFPKTEAFLLVAIQWSEARF 181  
 DB 121 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDFPKTEAFLLVAIQWSEARF 180  
 QY 182 KYIENQVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIYL 241  
 DB 181 KYIENQVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIYL 240  
 QY 242 RVDEINRDVALLKYVNGTCOTT 263  
 DB 241 RVDEINRDVALLKYVNGTCOTT 262

## RESULT 3

QY 08S947 PRELIMINARY: PRT: 261 AA.  
 ID 08S947  
 AC 08S947:  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE PAP-S1 (Fragment).  
 GN PAP-S1.  
 OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
 NC NCBL\_TaxID=3527;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP Honjo E., Matanabe K.:  
 RT "Cloning of genomic DNA encoding two types of pokeweed antiviral  
 RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of  
 RT their recombinant proteins with other PAP isoforms."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB071854; BAB86349.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 261 261  
 SO SEQUENCE 261 AA; 29199 MW; D88B98BEFE1F989 CRC64;

Query Match 81.0%; Score 1099.5; DB 10; Length 261;  
 Best local Similarity 83.2%; Pred. No. 3.5e-84;  
 Matches 218; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITPDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVLOGANLK 61  
 DB 1 INTITPDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVLOGANLK 60  
 QY 62 TITLMLRRNNLYMGVSDPENGKCRHIFNDITSTERTVENTLCCSSSSRYAAMSINYN 121  
 DB 61 TITLMLRRNNLYMGVSDPYD-NKCRHIFNDITSTERTVENTLCCSSSNPRAKPINYN 119  
 QY 122 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDFPKTEAFLLVAIQWSEARF 181  
 DB 120 GLVPTLEKKAAGVSRNOVQGIOLSSDICKISGVDFTEKFAKLLVAIQWSEARF 179  
 QY 182 KYIENQVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIYL 241  
 DB 180 KYIENQVKTNFNDFPNPKVLDLEENMGKISAHNNAKNGALPKPLEVDAGTKWIYL 239  
 QY 242 RVDEINRDVALLKYVNGTCOTT 263  
 DB 240 RVDEIKPDVGLLVNGTCOAT 261

## RESULT 4

QY 0941G8 PRELIMINARY: PRT: 313 AA.  
 ID 0941G8  
 AC 0941G8:  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE rRNA-24ycosidase (EC 3.2.2.22).  
 GN PAP.  
 OS Phytolacca aclinosa.  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
 NC NCBL\_TaxID=107615;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP Peng X., Yuan J., Qiang B.:  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AY049785; AAL15442.1;

DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 KW Hydrolase; Toxin.  
 SQ SEQUENCE 313 AA: 35059 MW: 6478ECD571C17885 CRC64:

Query Match 76.9%; Score 1044; DB 10; Length 313;  
 Best Local Similarity 76.0%; Pred. No. 2e-79;  
 Matches 199; Conservative 29; Mismatches 34; Indels 0; Gaps 0;

OY 2 INTTFDAGNTINKYATFMESLRNQAQDKPLKCYGIMLPDNTSTPKYLLVAGALNK 61  
 DB 23 VNTIYVNGSTTSTYATFELDLNREAKDPSLKGIMLPNTNPKYVLEVLQSSNKK 82  
 OY 62 TITLMLRRNNLYVGYSDPFGNCKRYHIFNDITSTERTDVENTLCCSSSSRYAMSIYN 121  
 DB 83 TITLMLRRNNLYVGYSDPFGTNCRCYHIFSDISTGERDVEITLCRPNRSKINNYD 142  
 OY 122 SLVPTMEKKAENVSRNOVGLGIISSDICKISGVDSFPVKTEAFELVAIQWSEARF 181  
 DB 143 SRYPLESKAGVSKRSQVQLGIIILDSNIGKISGVSTFTEKTEAEFLVAIQWSEARF 202  
 OY 182 KYIENOVKTNNRAFYDPKVINLEEKWKISIAIHAKNGALPKPLEVDAKGTWKIVL 241  
 DB 203 KYIGNOVKTNNRAFNPNPKVNLNEETWKGISTAIHDKNGLPKPLEVDASGAKWIVL 262  
 OY 242 RVDEINRDVALLKVYNGTCQTT 263  
 DB 263 RVDEIKRPDVALNLYVDSGTCQTT 284

RESULT 5  
 O9XFF8 PRELIMINARY: PRT: 315 AA.

AC O9XFF8: 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22).  
 GN Pip2.  
 OS Phytolacca insularis.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC NCBI\_TaxID=63744;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2050377; PubMed=11052196;  
 RA Song S.-K., Choi Y., Moon Y.H., Kim S.G., Choi Y.D., Lee J.S.;  
 RT "Systemic induction of a Phytolacca insularis antiviral protein gene  
 by mechanical wounding, jasmonic acid, and abscisic acid.";  
 RL Plant Mol. Biol. 43:439-450(2000).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC EMBL: AF141331; AAD32679.1; -  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR000396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; UNKNOWN\_1.  
 KW Hydrolase; Toxin.  
 SQ SEQUENCE 315 AA: 35728 MW: F85DE21154B5FA15 CRC64;

Query Match 72.0%; Score 977.5; DB 10; Length 315;  
 Best Local Similarity 74.0%; Pred. No. 7.3e-74;  
 Matches 194; Conservative 28; Mismatches 37; Indels 3; Gaps 3;

OY 3 NTTFDAGNATINKYATFMESLRNQAQDKPLKCYGIMLPDNTSTPKYLLVAGALNK 62  
 DB 28 NPITFEVGNATINKATFMKSLRDQAKDPNLCYCIPIMLPNTSLPKLVLVALQSSSLKT 87  
 OY 63 ITLMLRRNNLYVGYSDPFGNCKRYHIFNDIT-STERTDVENTLCCSSSSRYAMSIYN 121  
 DB 263 RVDEIKRPDVALNLYVDSGTCQTT 284

DB 88 ITLMLRRNNLYVGYADTYN-NKCRHYIFKDISNTTERNDVMTLCPNMSSRYGKNISYD 146  
 OY 122 SLVPTMEKKAENVSRNOVGLGIISSDICKISGVDSFPVKTEAFELVAIQWSEARF 181  
 DB 147 SSYPALEKKG-KRSRQVGLGIIILDSNIGKISGVSTFTEKTEAEFLVAIQWSEARF 205  
 OY 182 KYIENOVKTNNRAFYDPKVINLEEKWKISIAIHAKNGALPKPLEVDAKGTWKIVL 241  
 DB 206 KYIENOVKTNNRAFNPNPKVNLNEETWKGISTAIHDKNGLPKPLEVDASGAKWIVL 265  
 OY 242 RVDEINRDVALLKVYNGTCQTT 263  
 DB 266 RVDEIKRPDVALNLYVDSGTCQTT 287

RESULT 6  
 O8RYA4 PRELIMINARY: PRT: 339 AA.

AC O8RYA4: 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Ribosome inactivating protein type 1 precursor.  
 OS Phytolacca americana (Common pokeweed) (Virginiaian pokeweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Park S.-W., Lawrence C.B., Linden J.C., Vivanco J.M.;  
 RT "Characterization of a novel ethylene-inducible ribosome-inactivating  
 protein exuded from root cultures of Phytolacca americana.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY071928; AAL61546.1; -  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 339 AA: 37978 MW: 7D47BDC2DED965F CRC64;

Query Match 71.1%; Score 965; DB 10; Length 339;  
 Best Local Similarity 72.4%; Pred. No. 8.9e-73;  
 Matches 189; Conservative 22; Mismatches 46; Indels 4; Gaps 1;

OY 5 ITTFDAGNATINKYATFMESLRNQAQDKPLKCYGIMLPDNTSTPKYLLV-----KLGANL 60  
 DB 49 ISFDVGSATISKYTTFOESLRNQAQDKPLKCYGIMLPDNTSTPKYLLVLEIRAKLSTSEV 108  
 OY 61 KTTLMLRRNNLYVGYSDPFGNCKRYHIFNDITSTERTDVENTLCCSSSSRYAMSIYN 120  
 DB 109 KTTLMLRRNNLYVGYSDPIDVKKCRFHTEKDISGTERDQVETTLCPDPSRIKDIY 168  
 OY 121 NSLPTMEKKAENVSRNOVGLGIISSDICKISGVDSFPVKTEAFELVAIQWSEARF 180  
 DB 169 DSRYPJMETKAGVSGSOVGLGLEILNSGIGKISGVSTFTEKTEAEFLVAIQWSEARF 228  
 OY 181 FKYEIENOVKTNNRAFYDPKVINLEEKWKISIAIHAKNGALPKPLEVDAGKTWKIV 240  
 DB 229 FKYEIENOVKTNNRAFNPNPKVNLNEETWKGISTAIHDKNGLPKPLEVDASGAKWIV 288  
 OY 241 RVDEINRDVALLKVYNGTCQ 261  
 DB 289 RVDEIKSDVGLKLVYTGSCQ 309

RESULT 7  
 O9ATB3 PRELIMINARY: PRT: 237 AA.

AC O9ATB3: 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22) (Fragment).  
 GN MPAP.



```

OC Phytolacca americana (Common pokeweed). (Virgillian pokeweed).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen D., Wang X., Zhou G.:
RT "Pekeweed antiviral protein gene, partial cds."
RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADEOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF388910; AAK21951.1; -.
DR HSSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; toxin.
FT NON_TER 1 237
FT TER 237
SQ SEQUENCE 237 AA; 26534 MW; FE4ADCE03464783 CRC64;

Query Match 70.2%; Score 953; DB 10; Length 237;
Best Local Similarity 75.9%; Pred. No. 5.7e-72;
Matches 180; Conservatve 26; Mismatches 31; Indels 0; Gaps 0;

QY 2 INTTFDGNATINKKATPFMESLRNOADPKLKCGIMLPDPTNSTPKYLVLKOGANLK 61
Db 1 VNTIITVNGSTTISKYATFLDNLNREAKDPSLKCYGIMLPRTINPNRYVLVELOGSNKK 60
QY 62 TITMLRNNLVYGVSDPFNGKCRHYIFNDITSTERTDVENTLCSSSSSRVAMSIYN 121
Db 61 TITMLRNNLVYGVSDPFNGKCRHYIFNDITSTERTDVENTLCSSSSSRVAMSIYNFD 120
QY 122 SLVFTMEKKAENVNRNOVGLGIIQLSDIGKISGVDPKVTAEFLLVAIQMSEARF 181
Db 121 SRVFTLESKAGVKRSRQVGLGIIQLSDIGKISGVMSFTETKTEAEFLLVAIQMSEARF 180
QY 182 KYIENQVKTNRNRFYDPDKYINLEEKMGKTSAPAHNNKNGALPKRELVDAGKTKW 238
Db 181 KYIENQVKTNRNRFNPNKVLNLOETWGRKSTAHGKNGVLPKRELVDVDSAGRW 237

RESULT 8
P93077 PRELIMINARY: PRT: 302 AA.
AC P93077;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
GN R1P.
OS Clerodendrum aculeatum.
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Asteridae: euasterids I; Lamiales: Lamiaceae: Clerodendrum.
OX NCBI_TaxID=54208;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97238481; Pubmed=9132066;
RA Kumar D., Verma H.N., Tuteja N., Tewari K.K.:
RT "Cloning and characterisation of a gene encoding an antiviral protein
RT from Clerodendrum aculeatum L.;"
RL Plant Mol. Biol. 33:745-751(1997).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADEOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: X96474; CA65328.1; -.
DR EMBL: X96583; CA65402.1; -.
DR HSSP: P10297; 10CG.
```

```

DR      InterPro: IPR001574; RIP.
DR      Pfam: PF00161; RIP; 1.
DR      PRINTS: PR00396; SHIGARICIN.
DR      PROSITE: PS00275; SHIGA_RICIN; 1.
DR      Glycosidase: Hydrolase; Toxin.
KW      SEQUENCE 302 AA; 33955 MW; B0561C918C2E6A2 CRC64;

Query Match          51.7%; Score 701; DB 10; Length 302;
Best Local Similarity 56.1%; Pred. No. 9.7e-51;
Matches 143; Conservative 31; Mismatches 79; Indels 2; Gaps 2;

OY      7  FDAGNATINKATMEDIEMSRNADKPKLVCYGIPIMLPOTNSPKYLVLKQGANLKTITLM 66
DB      30  FHVAGATISITITTEINTLREAAKASLSCYGIPIMLPTTQPKHYLRLDADAATTITLI 89
OY      67  LRRNLVLVYGSDPFNGKRCRYHIFNDITSTERDVENTLCCSSSSSRVAMSINNSLYPT 126
DB      90  YNRNLNLVYLGSDFNG-ECRYHIFSDVGRGDRLEADDTLCPDENRQKQINIESNYS 148
OY      127 MEKKAENVSRNOVOLGIOLISSDIGKISGVDSFPVKTEAFPLVLAIQMVSAAKPKYIEN 186
DB      149 MENKAG-KSRQQLDELGINILTKSSIEKISGVAFRAFEKVEAEFLVLAIQMTAAARKYIEN 207
OY      187 QVKNENRRAFPDPKVINLEEKMKGISAHINANGALPKLELVDAKGTWYLRDEI 246
DB      208 LVKTNFNRFNFPDHRKMLRELTLTWKISTPIRNAONGVISPILNLSGDEPMWTVRDEI 267
OY      247 NRDAVLLKYVNGTCO 261
DB      268 KPYTALLNFNGSTCO 282

RESULT 9
ID      P93261          PRELIMINARY:      PRT:      289 AA.
AC      P93261;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DT      01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      rRNA-glycosidase (EC 3.2.2.22).
GN      RRP.
OS      Mesembryanthemum crystallinum (Common Ice plant).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
OX      NCBI_TaxID=3544;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98087998; PubMed=9426592;
RA      Rippman J.F., Michalowski C.B., Nelson D.E., Bohnerl H.J.;
RT      "Induction of a ribosome-inactivating protein upon environmental
RT      stress.";
RL      Plant Mol. Biol. 35:701-709(1997).
CC      -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC      SPECIFIC ADENOSINE ON THE 28S RNA.
CC      -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR      EMBL: U80072; AAB96824.1; ..
DR      HSSP: P10297; 10CG.
DR      InterPro: IPR001574; RIP.
DR      Pfam: PF00161; RIP; 1.
DR      PRINTS: PR00396; SHIGARICIN.
KW      Glycosidase; Hydrolase; Toxin.
SQ      SEQUENCE 289 AA; 32652 MW; 132AA996FBA27F1D CRC64;

Query Match          31.4%; Score 425.5; DB 10; Length 289;
Best Local Similarity 39.1%; Pred. No. 1.1e-27;
Matches 100; Conservative 44; Mismatches 105; Indels 7; Gaps 4;

OY      4  TTFDAGNATINKATMEDIEMSRNADKPKLVCYGIPIMLPOTNSPKYLVLKQGANLKT 63
DB      1  TTFDAGNATINKATMEDIEMSRNADKPKLVCYGIPIMLPOTNSPKYLVLKQGANLKT 63
OY      23  TLVLIDIGCATIEKTYSDPTKTLRTAEKKDRMYAVGLSMMPKPKPTTLVLVIKSKDMST 82
DB      64  TLMLRRNNLVLVYGSDPFNGKRCRYHIFNDITSTERDVENTLCCSSSSSRVAMSINNSL 123

```

```

Db      83 TLSSLRNDLVVGGISDMYK-KCRYHVEPHDSKPPYECHSLCDKKAIRKPIGVSS 141
QY      124 YPTMEKKAEVNSRNOVLOGIOLSSDICKISGVDFPVKTEAFELVAIOMVSPARFKY 183
Db      142 YTEIERAKARNKEIGLGVKNKLTLPKYYGSESKDYODEAFELVAITITAEARFPY 201
QY      184 IENOVKTENFRAPYPPPKVINLEEKWKCKISEAIIHNAKNGALPPLELVDAKGTWIVLRV 243
Db      202 IEKIAETAAAN-----PDTAICLENMWSKISKETIYNQKGNPOTPAKDVTRTCK-NLKG 256
QY      244 DEINRDVALLKYNGT 259
Db      257 NOVOKYITLLSY-OGT 271

```

## RESULT 10

```

Q9M5K6 PRELIMINARY; PRT; 279 AA.
AC Q9M5K6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE rRNA - glycosidase (EC 3.2.2.22).
GN CAP30A.
OS Chenopodium album (Lamb's-quarters).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiales; Chenopodium.
OX NCBI_TaxID=3559;
RN [1]
RP SEQUENCE FROM N.A.
RA Park J.S., Cho K.J., Lee S.M., Kim Y.T., Hwang Y.S.;
RT "A cDNA clone encoding a novel ribosome inactivating protein from
RT Chenopodium album L."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
DR EMBL: AF228508; AAF6234.1; -.
DR HSSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHIGARICIN.
DR HydroLase; Toxin.
SQ SEQUENCE 279 AA: 31377 MW: 2A53300E445DC952 CRC64;

```

Query Match 29.1%; Score 395; DB 10; Length 279;

Best Local Similarity 40.1%; Pred. No. 3.6e-25;

Matches 101; Conservative 37; Mismatches 96; Indels 18; Gaps 8;

```

QY      13 TINKYATFESLBNQAKDPKLCYGIPLPDTNSTPKYLLVKGQ---NLKTTTLMRLR 69
Db      37 TONTYTFLOSINQAKDPSLYEGIPMIRAPTNPTIILVELSKKNNEISITLALSR 96
QY      70 NNLVYGVSDPENGKCRHYIFNDITSTERTDVENTLCSSSSRVMSINVSLEYTMEK 129
Db      97 NDLVYVAADKF-GGKVRGHYFKNL-GISTDEANKVFPVVOFI--NITYGSEYNQIES 152
QY      130 KAEVNSRNOVLOGIOLSSDICKISGVDFP---VTEAFELVAIOMVSEARFYIEN 186
Db      153 NGGTN-RLSEPLGFDLTKYSRNKVVYGMPTTGGYSTETEARFLIAIOMVAEARFYIOG 211
QY      187 Q--VKTNFRAPYPPPKVINLEEKWKCKISEAIIHNAKNGALPPLELVDAKGTWIVLRV 244
Db      212 RAIVTTAPN-----DKIITSLNMGALSKGINNAKKYVNPITITLOYPDGKFWITVOS 266
QY      245 EINRDVALLKYV 256
Db      267 DVKNDMGLLKYV 278

```

RESULT 11

```

Q39418 PRELIMINARY; PRT; 272 AA.
AC Q39418;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Antiviral protein precursor (Ribosome-inactivating protein) (RNA N-
DE glycosidase) (Polynucleotide:adenosine glycosidase) (EC 3.2.2.22)
DE (BETAVULGIN) (BVG).
GN RIP OR BETAVULGIN OR BVG.
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiales; Beta.
OX NCBI_TaxID=3559;
RN [1]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RC TISSUE-SEEDLING;
RX MEDLINE=96235141; PubMed=8666251;
RA Horning E., Majant H., Jeske H., Mundry K.-W.;
RT "Cloning of a cDNA encoding a new ribosome-inactivating protein from
RT Beta vulgaris vulgaris (mangold).";
RL Gene 170.233-236(1996).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS. AND PROTEIN
CC SYNTHESIS IN VITRO. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR
CC SUICIDE UPON INVASION BY A VIRUS.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
CC PROTEINS.
CC -1- SIMILARITY: BELONGS TO TYPE 1 RIP.
DR EMBL: X85967; CAAS9952.1; -.
DR HSSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; FALSE_NEG.
DR HydroLase; Glycosidase; Antiviral; Protein synthesis inhibitor; Toxin;
KW Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 272 ANTIVIRAL PROTEIN.
FT ACT_SITE 196 196 BY SIMILARITY.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 272 AA: 30168 MW: 77DD0917FD12FDFE CRC64;

```

Query Match 29.0%; Score 394; DB 10; Length 272;

Best Local Similarity 40.5%; Pred. No. 4.2e-25;

Matches 105; Conservative 36; Mismatches 98; Indels 20; Gaps 7;

```

QY      5 IFPDAGNATINKYATFESLBNQAKDPKLCYGIPLPDTNSTPKYLLVKGQ---GANL 60
Db      26 VTFDELTAASKTCTGLSNLRNIVKSKLYVEDIPMIPAIKAKILLAEKAKKAGTQI 85
QY      61 KTTTLMRLNRLVYGVSDPENGKCRHYIFNDITSTERTDVENTLCSSSSRVMSINVS 120
Db      86 -TTTAVSKNDLVVAVFTDQVAG-KLRARHYFPDISLATAKAIPPT-----AVQYIOIG 137
QY      121 NSLYPTMEKKAEVNSRNOVLOGIOLSSDICKISG---VDSFPVKTEAFELVAIOMVSE 177
Db      138 TSNVYSIEGAAGSN-RVNFQLGFKVLEKYEYMLVYGNVQDSRRSEARFLAAIOMVAE 196
QY      178 AARFYKTIENOVKTENFRAPYPPPKVINLEEKWKCKISEAIIHNAKNGALPPLELVDAKGT 237
Db      197 AARFYKVESAIANN-----VVPDKYVSLNENMSKISEGICRAKAKKYISPITELVANSNGK 252
QY      238 WIVLRVDEINRDVALLKYV 256
Db      253 WTVNVOVSDIKPDGILSYV 271

```

## RESULT 12

Q9A0E3 PRELIMINARY; PRT; 279 AA.

AC 09AUE3;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE rRNA - glycosidase (EC 3.2.2.22).  
 OS CAP30B.  
 GN Chenopodium album (Lamb's-quarters).  
 ON Chenopodiaceae: Chenopodiales; Chenopodium.  
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium.  
 NC NCBI\_TaxID:3559;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Park J.S., Lee S.M., Kim Y.T., Cho K.J.;  
 RT Molecular characterization of a new cDNA clone encoding a ribosome-  
 inactivating protein (CAP30B) from Chenopodium album."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOTOXINOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AF230812; AAK28323.1;  
 DR HSSP: 003464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP.1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR Hydrolase: Toxin.  
 SQ SEQUENCE 279 AA: 31419 MW: 97E93AF22C8033AF CRC64;  
 Query Match 28.2%; Score 382; DB 10; Length 279;  
 Best Local Similarity 39.1%; Pred. No. 4.4e-24;  
 Matches 99; Conservative 42; Mismatches 92; Indels 20; Gaps 8;  
 QY 13 TINKYATFESLRNOKADPKLCYGIPLMPDFTNTPKYLVLKOGA---NLKTTTLMRLR 69  
 ID 093Y64; PRELIMINARY; PRT; 294 AA.  
 AC 093Y64;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DE rRNA - glycosidase (EC 3.2.2.22).  
 OS Dianthus chinensis.  
 GN Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Caryophyllaceae; Dianthus.  
 NC NCBI\_TaxID:118431;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20306826; Pubmed-10850653;  
 RT "Isolation and characterization of cDNAs encoding ribosome  
 inactivating protein from Dianthus sinensis L.";  
 RL Mol. Cells 10:135-141(2000).  
 QY 266 SDVKNMDGLLKYV 278  
 DB 211 GRAYVTAR-----NRYIVSELTNMGALSCKGRNAYKVINPITLQYPDGKTWIVTQY 265  
 QY 244 DEINRDVALLKYV 256  
 DB 152 TNAGTN-RISFPLGFMNLTFTNKYKVGDMPTKAGNYTQTEKFLLIADIONVAEAKREKYIE 210  
 QY 129 KKAENVSRNOVOLGIIOLSSDICKISGVDSF---VKTEFELVLAIQWSEAKREKYIE 185  
 DB 186 NQ--VKTNENRAFYPPDKVINLEEKWKISEAHNKNGALPPLVLAQAKGKWLVRV 243  
 QY 211 GRAYVTAR-----NRYIVSELTNMGALSCKGRNAYKVINPITLQYPDGKTWIVTQY 265  
 QY 244 DEINRDVALLKYV 256  
 DB 266 SDVKNMDGLLKYV 278

CC -1- CATALYTIC ACTIVITY: ENDOTOXINOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AF219237; AAK68928.1;  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP.1.  
 DR Hydrolase: Toxin.  
 SQ SEQUENCE 294 AA: 33331 MW: 659E72DD847A72D0 CRC64;  
 Query Match 24.2%; Score 328; DB 10; Length 294;  
 Best Local Similarity 37.4%; Pred. No. 1.6e-19;  
 Matches 88; Conservative 37; Mismatches 92; Indels 18; Gaps 8;  
 QY 2 INTITFDAGNATINKATFESLRNOKADPKLCYG--IPMLPDTNTPKYLVLKOGAN 59  
 DB 25 VRTFTDLARPTAAKSSFLDQIRNNMRPRLKYSTELAVIKAPSVADKFLRINQGR 84  
 QY 60 LKTTITLMRRNLVWGYSDPFGNKKCR-YHIFNDITSTERTDY--ENTLCSSSSSRVAM 116  
 DB 85 -GTVSLGLARVNLVYAVFAVDNRNVRNAYFRTEINSAELTVPPEVIVANQ-----R 137  
 QY 117 SINYNGLPYTMEKKAEV---NSRNOVOLGIIOLSSDICKISGVDSFPYKTEAFVLVAI 172  
 DB 138 PLETTEDYOSIEKNNAKITTGDKSRKELGICIDLLISTIDKVKKKRV-VKDEARFLLCI 196  
 QY 173 QWSEAKREKYIENOVKTNENRAFYPPDKVINLEEKWKISEAHNKNGALPK 226  
 DB 197 QMSAEAVFRYIONLVTBNPKKFNEDNTVIOYQTSWKISEAHSCKNGKFNK 251  
 RESULT 14  
 Q93Y64  
 ID 093Y64; PRELIMINARY; PRT; 294 AA.  
 AC 093Y64;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DE rRNA - glycosidase (EC 3.2.2.22).  
 OS Dianthus chinensis.  
 GN Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Caryophyllaceae; Dianthus.  
 NC NCBI\_TaxID:118431;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20306826; Pubmed-10850653;  
 RT "Isolation and characterization of cDNAs encoding ribosome  
 inactivating protein from Dianthus sinensis L.";  
 RL Mol. Cells 10:135-141(2000).  
 CC -1- CATALYTIC ACTIVITY: ENDOTOXINOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AF219238; AAK68929.1;  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP.1.  
 DR Hydrolase: Toxin.  
 SQ SEQUENCE 294 AA: 33267 MW: E196CE3F1DF97C82 CRC64;  
 Query Match 24.2%; Score 328; DB 10; Length 294;  
 Best Local Similarity 37.4%; Pred. No. 1.6e-19;  
 Matches 88; Conservative 37; Mismatches 92; Indels 18; Gaps 8;  
 QY 2 INTITFDAGNATINKATFESLRNOKADPKLCYG--IPMLPDTNTPKYLVLKOGAN 59  
 DB 25 VRTFTDLARPTAAKSSFLDQIRNNMRPRLKYSTELAVIKAPSVADKFLRINQGR 84  
 QY 60 LKTTITLMRRNLVWGYSDPFGNKKCR-YHIFNDITSTERTDY--ENTLCSSSSSRVAM 116  
 DB 85 -GTVSLGLARVNLVYAVFAVDNRNVRNAYFRTEINSAELRTPPEVIVANQ-----R 137  
 QY 117 SINYNGLPYTMEKKAEV---NSRNOVOLGIIOLSSDICKISGVDSFPYKTEAFVLVAI 172

Db 138 PLEYEDYOSIEKNATTGDKSRKELGIDLLISTIDKVNKKVRV-VKDEARFLLIGI 196

OY 173 QMVSARFERYIENOVKTENFNAFYPPDKYINLEEKWKISEAIIH-NAKNGALPK 226

Db 197 QMSAEAVRFYIENLVTRNFPKKNKNSDNTYIOYOTSMGKISEAIIHSDCKKNGKFNK 251

## RESULT 15

Q9S9E4 PRELIMINARY: PRT: 258 AA.

AC Q9S9E4: 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE rRNA -glycosidase (EC 3.2.2.22).

OS Gelonium multiflorum (Euphorbiaceae himalay).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Malpighiales; Euphorbiaceae; Gelonium.

OX NCBI\_taxID=3979;

RN [1]

RP SEQUENCE.

RX MEDLINE=96006751; PubMed=755324;

RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,

RT Toman P.D., Cheung L.;

RT "Amino acid sequence analysis, gene construction, cloning, and

RT expression of gelonin, a toxin derived from Gelonium multiflorum.";

RL J. Interferon Cytokine Res. 15:547-555(1995).

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.

CC HSSP: P09989; IMRJ.

DR InterPro: IPR001574; RIP.

DR Pfam: PF00161; RIP.1.

DR PRINTS: PR00396; SHIGARICIN.

KW Hydrolase; Toxin.

SO SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 23.7%; Score 321.5; DB 10; Length 258;

Best Local Similarity 32.5%; Pred. No. 4,6e-19;

Matches 86; Conservative 50; Mismatches 108; Indels 21; Gaps 8;

OY 2 INTITFDAGNATINKYATMESIRNQAKDPKLCYGIPLMLPTNSTPK-YLLVYKOGANL 60

Db 2 LDTVSESTGATYITVNFLELRVYK-L-PEGNSHGIPLLRKGDDPGKCFVALSNDNG 60

OY 61 KTTITLMLRRNNLYVMGYSDFPENGKCRHYHENDITSTE----RTDVENTLCSSSSRYA 115

Db 61 QLAETIAIDVTSYVVGQ-----VRNRSYFFKDPADPAAYEGLEFKNTIKNPFLFGKTR-- 113

OY 116 MSINYSLYPTMEKKAENSRNOVQGLIOLSSDICKI--SGVDSFPVKTAEFFLLVAIO 173

Db 114 --LHFGSGYPSLE--GEKAYRETTDGIETPLRIGIKKLDENAIQNKPTETIASLLVIO 169

OY 174 MVSSEARFERYIENOVKTENFNAFYPPDKYINLEEKWKISEAIIH-NAKNGALPKPLEYD 232

Db 170 MVSSEARFERYIENOVKTENFNAFYPPDKYINLEEKWKISEAIIH-NAKNGALPKPLEYD 232

OY 233 AKGTKWIYLRVDEINDVALLKYVN 257

Db 230 ANGKKIYVAVDQVKPKIALKFVD 254

Search completed: July 2, 2003, 11:42:08

Job time : 40.044 secs



Sequence 4, Application US/09978274A  
Patent No. US20020116737A1  
GENERAL INFORMATION:  
APPLICANT: Thomas, Christopher  
APPLICANT: McPherson, Michael  
APPLICANT: Atkinson, Howard  
APPLICANT: Neelam, Anil  
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM  
FILE REFERENCE: 9341-028  
CURRENT APPLICATION NUMBER: US/09/978,274A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0025225.4  
PRIOR FILING DATE: 2000-10-14  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 263  
TYPE: PRF  
ORGANISM: Phytolacca americana  
US-09-978-274A-4

Query Match 100.0%; Score 793; DB 10; Length 263;  
Best Local Similarity 100.0%; Pred. No. 2,7e-77;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MINTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 60  
DB 1 MINTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 60  
QY 61 KITTLMLRRNNLYVWGSDPFGNKCRIHFNDITSTERTDVENTLSCSSSSRVAMSIYN 120  
DB 61 KITTLMLRRNNLYVWGSDPFGNKCRIHFNDITSTERTDVENTLSCSSSSRVAMSIYN 120  
QY 121 NSLYPTMEKKAEVNSRNOVOLGIQLSSDIGKIS 154  
DB 121 NSLYPTMEKKAEVNSRNOVOLGIQLSSDIGKIS 154

RESULT 3  
US-09-978-274A-2  
Sequence 2, Application US/09978274A  
Patent No. US20020116737A1  
GENERAL INFORMATION:  
APPLICANT: Thomas, Christopher  
APPLICANT: McPherson, Michael  
APPLICANT: Atkinson, Howard  
APPLICANT: Neelam, Anil  
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM  
FILE REFERENCE: 9341-028  
CURRENT APPLICATION NUMBER: US/09/978,274A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0025225.4  
PRIOR FILING DATE: 2000-10-14  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 314  
TYPE: PRF  
ORGANISM: Phytolacca americana  
US-09-978-274A-2

Query Match 99.4%; Score 788; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1,2e-76;  
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 61  
DB 25 INTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 61  
QY 62 KITTLMLRRNNLYVWGSDPFGNKCRIHFNDITSTERTDVENTLSCSSSSRVAMSIYN 121  
DB 85 KITTLMLRRNNLYVWGSDPFGNKCRIHFNDITSTERTDVENTLSCSSSSRVAMSIYN 144

QY 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDIGKIS 154  
DB 145 SLVPTMEKKAEVNSRNOVOLGIQLSSDIGKIS 177

RESULT 4  
US-09-792-793A-85  
Sequence 85, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 85  
LENGTH: 254  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Methionine-Saporin fusion  
US-09-792-793A-85

Query Match 24.8%; Score 196.5; DB 9; Length 254;  
Best Local Similarity 31.9%; Pred. No. 3,6e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 59  
DB 1 MINTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 59  
QY 60 KITTLMLRRNNLYVWGSDPFGNKCRIHFNDITSTERTDVENTLSCSSSSRVAMSIYN 118  
DB 61 KITTLMLRRNNLYVWGSDPFGNKCRIHFNDITSTERTDVENTLSCSSSSRVAMSIYN 118  
QY 119 NYSLYPTMEKKAEVNSRNOVOLGIQLSSDIGKIS 154  
DB 116 EYTEDYOSIEKNAOITGDSQRKELGIDLSTSMENVN 155

RESULT 5  
US-09-792-793A-79  
Sequence 79, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 79  
LENGTH: 327  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion pro  
US-09-792-793A-79

Query Match 24.8%; Score 196.5; DB 9; Length 327;  
Best Local Similarity 31.9%; Pred. No. 5,1e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 59  
DB 1 MINTTFDAGNATINKYATFMSLRNQAADPKLKCIGIPMLPDTNSTPKYLLVKGANL 59

Db 74 MVTSTLTLVPTAGVSSFDVKIRNNKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 133  
QY 60 LKTTTLMRLNNLVYMGSDPFNGNCKR-YHIFNDITSTERTDVENTLSCSSSSRVAMSI 118  
Db 134 -GTVSLGKRDNLVVAIVLAMDNTNVRAYFRSEITSAEST---ALFPEATANOKAL 188  
QY 119 NYSLYPTMEKKAEV---NSRNOVOLGIQLSSDICKIS 154  
Db 189 EYTEDYOSIEKNAQITOGDSRKELGIGIDLSTSM EAVN 228

## RESULT 6

US-09-792-793A-82  
Sequence 82, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 82  
LENGTH: 330  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion prote  
US-09-792-793A-82

Query Match 24.8%, Score 196.5; DB 9; Length 330;  
Best Local Similarity 31.9%, Pred. No. 5.1e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTITPDAGNATINKYATFMSLRNQAQDKPKLCYGPMLPPTNSTPKYLVLKLOGAN 59  
Db 77 MVTSTLTLVPTAGVSSFDVKIRNNKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 136  
QY 60 LKTTTLMRLNNLVYMGSDPFNGNCKR-YHIFNDITSTERTDVENTLSCSSSSRVAMSI 118  
Db 137 -GTVSLGKRDNLVVAIVLAMDNTNVRAYFRSEITSAEST---ALFPEATANOKAL 191  
QY 119 NYSLYPTMEKKAEV---NSRNOVOLGIQLSSDICKIS 154  
Db 192 EYTEDYOSIEKNAQITOGDSRKELGIGIDLSTSM EAVN 231

## RESULT 7

US-09-792-793A-73  
Sequence 73, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 73  
LENGTH: 332  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion prote  
US-09-792-793A-73

Query Match 24.8%, Score 196.5; DB 9; Length 332;  
Best Local Similarity 31.9%, Pred. No. 5.2e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTITPDAGNATINKYATFMSLRNQAQDKPKLCYGPMLPPTNSTPKYLVLKLOGAN 59  
Db 79 MVTSTLTLVPTAGVSSFDVKIRNNKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 138  
QY 60 LKTTTLMRLNNLVYMGSDPFNGNCKR-YHIFNDITSTERTDVENTLSCSSSSRVAMSI 118  
Db 139 -GTVSLGKRDNLVVAIVLAMDNTNVRAYFRSEITSAEST---ALFPEATANOKAL 193  
QY 119 NYSLYPTMEKKAEV---NSRNOVOLGIQLSSDICKIS 154  
Db 194 EYTEDYOSIEKNAQITOGDSRKELGIGIDLSTSM EAVN 233

## RESULT 8

US-09-792-793A-76  
Sequence 76, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 76  
LENGTH: 332  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion pr  
US-09-792-793A-76

Query Match 24.8%, Score 196.5; DB 9; Length 332;  
Best Local Similarity 31.9%, Pred. No. 5.2e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTITPDAGNATINKYATFMSLRNQAQDKPKLCYGPMLPPTNSTPKYLVLKLOGAN 59  
Db 79 MVTSTLTLVPTAGVSSFDVKIRNNKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 138  
QY 60 LKTTTLMRLNNLVYMGSDPFNGNCKR-YHIFNDITSTERTDVENTLSCSSSSRVAMSI 118  
Db 139 -GTVSLGKRDNLVVAIVLAMDNTNVRAYFRSEITSAEST---ALFPEATANOKAL 193  
QY 119 NYSLYPTMEKKAEV---NSRNOVOLGIQLSSDICKIS 154  
Db 194 EYTEDYOSIEKNAQITOGDSRKELGIGIDLSTSM EAVN 233

## RESULT 9

US-09-792-793A-35  
Sequence 35, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 35

```

; LENGTH: 275
; TYPE: PRT
; ORGANISM: Saponaria officinalis
US-09-792-793A-35

```

Query Match	24.18;	Score 191.5;	DB 9;	Length 275;
Best Local Similarity	31.48;	Pred. No. 1.4e-12;		
Matches 50;	Conservative 37;	Mismatches 61;	Indels 11;	Gaps 5

QY INITITDEAANAATINKATMETESLRQAQDPKCKCGIDM-LPTDINSPIKYLLVQLQCANL 60  
 :  
 Db 1 VTSITLDLVNPAAGQSSFVDKIRNNVADPNLKLYGTGTAIVICGPPEKKFKIIRFOSSR- 59  
  
 QY 61 KTTTLRRNNLTVMGYSDPFNGKRC-YHIFNDTSTERTDVENTLCSSSSSVAMSIIN 119  
 :  
 Db 60 GTVSLGLGRDLNYVAAYLAMDMNTNVNRAFYFRSEITSNEST-----ALPPEATTNKALE 115  
  
 QY 120 YNSLYPTMEKKAEEV---NSRNQVQLGIQLLSSDQIKS 154  
 | | | :  
 Db 116 YTDEDYSIEKNNOITOGDOSRKELDGLDLASTISHEAVN 154

RESULT 10  
US-09-792-793A-36  
; Sequence 36, Application US/09792793A  
; Patent No. US20020168370A1

```

: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 36
: LENGTH: 250
: TYPE: PR1
: ORGANISM: Momordica charantia
: US-09-792-793A-36

```

	Query Match	15.1%	Score 120;	DB 9;	Length 250;	
	Best Local Similarity	28.8%	Pred. No. 6e-05;			
	Matches	44;	Conservative	26;	Mismatches	71; Indels 12; Gaps 7
OY	2 INTI-TFDIGNATINKATATEMESLNRQADKCLKCYGIMLPDPTNSTPKYLKLGANTL	60				
	: : : : : : : : : : : : : : : :					
Db	4 LEETIASLDLNPP--TYSLFITNIRTKVADKEQC-FIQRSKR-FIQRRSYIDLVSST	59				
	: : : : : : : : : : : : : : : :					
OY	61 KTTTLMLRNNLVWGYSDPFENGKKCRHINDDITSTERDVENTLCSSSSRYAMSINY	120				
	: : : : : : : : : : : : : : : :					
Db	60 OKRTLAIDMADLYVGSGDIAN-NKGRAFFEKDVTEA---VANNEFPFAGTNRIKLTF	114				
	: : : : : : : : : : : : : : : :					
OY	121 NSLYPTMEKKAEVNSRNVOGLQIOLSSDICKI	153				
	: : : : : : : : : : : : : : : :					
Db	115 TCSYGDLKENGGLRKDN--PLGIIFRLKSIVNI	145				

```

RESULT 11
US-09-792-793A-34
: Sequence 34, Application US/09792793A
: Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Cogdins, Phillip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 34
; LENGTH: 247
; TYPE: PR1
; ORGANISM: Bryonia dioica
US-09-792-793A-34

```

Query Match	14.1%;	Score 111.5;	DB 9;	Length 247;
Best Local Similarity	26.8%;	Pred. No. 0.00048;		
Matches 40;	Conservative 31;	Mismatches 61;	Indels 17;	Gaps 7;

QY 5 IITDAENNAIINKATFMEELRNQARDPKKCYGIMEDDT -NSPPKLVKLGQANAKTI 63  
 Db 2 VSFRLSGAATTSXGYFIKNLR -EALPYEKVYINIPILLSSISGGRYTLHLITVYADETI 60  
 QY 64 TLLRLNNLIYVNGYSDPFNGKRCRAHYIFNDITSTERTDVENTLSSSSRYAM -SINY 121  
 Db 61 SVAVDVTNYINGY --LAGDVS -YFFNEASATE ---AAKFVRKDKKKKVTLPYSNTE 112  
 QY 122 SLPTMEKKAENVSRNVOIGQLSSDI 150  
 Db 113 RL-----OTACKIRINIPGLPALDSAI 136

RESULT 12  
US-09-765-527-259  
; Sequence 259, Application US/09765527  
; Patent No. US20020006638A1

TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
 Fusion Proteins and BPI-Derived Peptides  
 NUMBER OF SEQUENCES: 265  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/765,527  
 FILING DATE: 18-Jan-2001  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/621,803  
 FILING DATE: 01-18-1994

```

ATTORNEY/AGENT INFORMATION:
? NAME: Borun, Michael F.
? REGISTRATION NUMBER: 25,447
? REFERENCE/DOCKET NUMBER: 27129/3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/474-6300
? TELEFAX: 312/474-0448
? TELEEX: 25-3856
? INFORMATION FOR SEQ ID NO: 259:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 293 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 259
US-09-765-527-239

```

Query Match	13.98;	Score 110.5;	DB 10;	Length 293;
Best Local Similarity	25.28;	Pred. No. 0.00078;		
Matches	39;	Conservative	29;	Mismatches 68; Indels 19; Gaps 6

2 INTTFDAGNATINKYATFMSLRNQADPKLKCYGIPMEEDNSTPK--YLVLKLGAN 59



Db 24 LDTVSFSTKCATIITYVNFLELRYKLK-PEGNSHGIPLLRKKCDPGKCFVLAISDN 82  
QY 60 LKTTTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDITSTERDV-ENTLCSSSSSRVAMSI 118  
Db 83 GOLAEIADIVTSYVVGQ-----VRNRSYFFKADPAAYEGLEFKNT-----IKTRL 129  
QY 119 NYSNLYPTMEKKAEVNSRNOVOLGIQLSSDIGKI 153  
Db 130 HFGGTYPSE--GEKAYRETTDLGIEPLRIGIKKL 162

## RESULT 13

US-09-765-527-253  
Sequence 253, Application US/09765527  
Patent No. US2002000638A1  
GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 253:  
US-09-765-527-253

Query Match 13.9%; Score 110.5; DB 10; Length 309;  
Best Local Similarity 25.2%; Pred. No. 0.00084;  
Matches 39; Conservative 29; Mismatches 68; Indels 19; Gaps 6;

QY 2 INTTPDAGNATIKKYATFMESLRNQAOKPKLCYGPMLPTNSTPK--YLLVKLOGAN 59  
Db 24 LDTVSFSTKCATIITYVNFLELRYKLK-PEGNSHGIPLLRKKCDPGKCFVLAISDN 82  
QY 60 LKTTTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDITSTERDV-ENTLCSSSSSRVAMSI 118  
Db 83 GOLAEIADIVTSYVVGQ-----VRNRSYFFKADPAAYEGLEFKNT-----IKTRL 129  
QY 119 NYSNLYPTMEKKAEVNSRNOVOLGIQLSSDIGKI 153  
Db 130 HFGGTYPSE--GEKAYRETTDLGIEPLRIGIKKL 162

RESULT 14

## US-09-765-527-251

Sequence 251, Application US/09765527  
Patent No. US2002000638A1  
GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 251:  
US-09-765-527-251

Query Match 13.9%; Score 110.5; DB 10; Length 332;  
Best Local Similarity 25.2%; Pred. No. 0.00092;  
Matches 39; Conservative 29; Mismatches 68; Indels 19; Gaps 6;

QY 2 INTTPDAGNATIKKYATFMESLRNQAOKPKLCYGPMLPTNSTPK--YLLVKLOGAN 59  
Db 24 LDTVSFSTKCATIITYVNFLELRYKLK-PEGNSHGIPLLRKKCDPGKCFVLAISDN 82  
QY 60 LKTTTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDITSTERDV-ENTLCSSSSSRVAMSI 118  
Db 83 GOLAEIADIVTSYVVGQ-----VRNRSYFFKADPAAYEGLEFKNT-----IKTRL 129  
QY 119 NYSNLYPTMEKKAEVNSRNOVOLGIQLSSDIGKI 153  
Db 130 HFGGTYPSE--GEKAYRETTDLGIEPLRIGIKKL 162

## RESULT 15

US-09-792-793A-39  
Sequence 39, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 39  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Trichosantheus killowii  
US-09-792-793A-39

Query Match 13.8%; Score 109.5; DB 9; Length 247;  
Best Local Similarity 27.8%; Pred. No. 0.00079;  
Matches 42; Conservative 29; Mismatches 59; Indels 21; Gaps 8;

QY	5	ITPDAGNATIKYATFMEISLBNQAKDPRKLCYCIPIMLPDTNSTP--KYLIVKIQANLK	61
DB	2	VSERLSGATSSSYGVFISNR-KALPNERKLYDIPLL-RSLPGSQRYALHILTNYADE	58
QY	62	TITMLRRNNLYVNGYSDPFNGNRCRYHIFNDITSTERTDVENTLCSSSSSRVAM--SIN	119
DB	59	TISVAIDVTNYIMGYR--AGDTS--YFNEASATE--AAKYVFKDAMRKVTLPYISGN	110
QY	120	YNSLYPTMEKKAENVSRNQVOLGIQILSSDI	150
DB	111	YERL-----QTAACKIRENIPGLPALDSAI	136

Search completed: July 2, 2003, 12:00:36  
Job time : 23.9717 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 9.92767 Seconds  
(Without alignments)  
456,414 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793  
Sequence: 1 MINTTFDAGNATINKYATF.....SRNOVOLGIQILSSDICKIS 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	667.5	84.2	261	1	US-08-378-761A-9 Sequence 79, Appl
2	667.5	84.2	261	1	US-08-485-286-79 Sequence 79, Appl
3	667.5	84.2	261	1	US-08-488-113B-9 Sequence 9, Appl
4	667.5	84.2	261	1	US-08-477-484B-9 Sequence 9, Appl
5	667.5	84.2	261	2	US-08-646-360-9 Sequence 9, Appl
6	667.5	84.2	261	4	US-08-839-765-9 Sequence 9, Appl
7	667.5	84.2	261	4	US-09-136-389-9 Sequence 9, Appl
8	667.5	84.2	261	4	US-09-610-838-9 Sequence 9, Appl
9	660.5	83.3	261	1	US-07-901-707-9 Sequence 9, Appl
10	660.5	83.3	261	1	US-07-988-430-9 Sequence 9, Appl
11	660.5	83.3	261	1	US-08-425-336-9 Sequence 9, Appl
12	660.5	83.3	261	5	PCT-US92-09487-9 Sequence 9, Appl
13	596	75.2	313	1	US-08-373-858-2 Sequence 2, Appl
14	596	75.2	313	1	US-08-500-611-2 Sequence 2, Appl
15	596	75.2	313	4	US-08-500-694-2 Sequence 2, Appl
16	596	75.2	313	4	US-09-005-273-2 Sequence 2, Appl
17	596	75.2	313	4	US-08-501-253A-2 Sequence 2, Appl
18	596	75.2	313	5	PCT-US96-11546-2 Sequence 2, Appl
19	588	74.1	313	4	US-09-005-273-4 Sequence 4, Appl
20	463.5	58.4	305	1	US-08-138-636-2 Sequence 2, Appl
21	463.5	58.4	305	1	US-08-319-622A-2 Sequence 2, Appl
22	463.5	58.4	305	1	US-08-471-564-2 Sequence 2, Appl
23	191.5	24.1	259	1	US-07-901-707-10 Sequence 10, Appl
24	191.5	24.1	259	1	US-07-988-430-10 Sequence 10, Appl
25	191.5	24.1	259	1	US-08-425-336-10 Sequence 10, Appl
26	191.5	24.1	259	1	US-08-488-113B-10 Sequence 10, Appl
27	191.5	24.1	259	1	US-08-477-484B-10 Sequence 10, Appl

28	191.5	24.1	259	2	US-08-646-360-10 Sequence 10, Appl
29	191.5	24.1	259	4	US-08-839-765-10 Sequence 10, Appl
30	191.5	24.1	259	4	US-09-136-389-10 Sequence 10, Appl
31	191.5	24.1	259	4	US-09-610-838-10 Sequence 10, Appl
32	191.5	24.1	259	5	PCT-US92-09487-10 Sequence 10, Appl
33	191.5	24.1	260	1	US-08-378-761A-72 Sequence 72, Appl
34	191.5	24.1	260	1	US-08-485-286-72 Sequence 72, Appl
35	169	21.3	292	1	US-08-378-761A-81 Sequence 81, Appl
36	169	21.3	292	1	US-08-485-286-81 Sequence 81, Appl
37	120	15.1	250	1	US-07-901-707-8 Sequence 8, Appl
38	120	15.1	250	1	US-07-988-430-8 Sequence 8, Appl
39	120	15.1	250	1	US-08-425-336-8 Sequence 8, Appl
40	120	15.1	250	1	US-08-488-113B-8 Sequence 8, Appl
41	120	15.1	250	1	US-08-477-484B-8 Sequence 8, Appl
42	120	15.1	250	2	US-08-646-360-8 Sequence 8, Appl
43	120	15.1	250	4	US-08-839-765-8 Sequence 8, Appl
44	120	15.1	250	4	US-09-136-389-8 Sequence 8, Appl
45	120	15.1	250	4	US-09-610-838-8 Sequence 8, Appl

#### ALIGNMENTS

```
RESULT 1
US-08-378-761A-79
; Sequence 79, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESS: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO. 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-761A-79

Query Match      84.2% Score 667.5; DB 1: Length 261;
Best Local Similarity 85.6% Pred. No. 2,2e+72;
Matches 131: Conservative 9; Mismatches 12; Indels 1; Gaps 1;
```

QY 2 INTTFDAGNATINKYATFMSLRNOAKPKLKCICGIPMLPDTNSTPKYLLVKGANKL 61  
DB 1 INTTFDAGNATINKYATFMSLRNEAKDPKLCYCIPMLPNTNSTTKYLLVKGASL 60

**Oy** 62 TITLMLRRNNLYVMGYSDFPENGKCRHAFHNDITSTETDVENTICSSSRVAMSYN 122  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
**Dd** 61 TITLMLRRNNLYVMGSDPYD-NKCRHYHFINDIKCTEYSDVENTLCPSNRRAKPLINYN 119  
.  
**Oy** 122 SLPTMEKKAEVNSRNOVGLOIILSSDGKTS 154  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
**Dd** 120 GLPTLEKKAGVTSRNEVOGLIOILSSDGKITS 152

## RESULT 2

```

Sequence 79, Application US/08485286
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-79

```

Query Match	84.2%	Score 667.5	DB 1:	Length 261:
Best Local Similarity	85.6%	Pred. No. 2.2e72:		
Matches 131:	Conservative 9:	Mismatches 12:	Indels 1:	Gaps 1
QY	2	INTITFDAGNATINKVATFMESLRNQAQDKPKCYGIMLPDNTSPKYLVLKLOGANLK	61	
Db	1	INTITFDAGNATINKVATFMESLRNEADPSLCKGIMLPNTNTIKYLLVKKLOGASLK	60	
QY	62	TITLMLRNRLNYWGYSDPFNGKCRHIFENDITSTERTDVENITLCSSSSRVAMISYN	121	
Db	61	TITLMLRNRLNYWGYSDPYD-NKCRHYHIFNDIKETESDVENITLCPSPNPRVAPRINYN	119	
QY	122	SLVPTMEKKAEVNSRNOVGLGILLSSIGKIS	154	
Db	120	GLVPTLEKKAGVTSRNEVGLGILLSSIGKIS	152	

### RESULT 3

: Sequence 9, Application US/08488113B  
 : Patent No. 574580  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Better, Marc D.  
 : APPLICANT: Carroll, Stephen F.  
 : APPLICANT: Cuduhika, Gary M.  
 : TITLE OF INVENTION: Immunitoxins Comprising Ribosome-Inactivating  
 : TITLE OF INVENTION: Proteins  
 : NUMBER OF SEQUENCES: 169  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 : STREET: 500 West Madison Street, 34th Floor  
 : CITY: Chicago  
 : STATE: Illinois  
 : COUNTRY: USA  
 : ZIP: 60661  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC Compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/488,113B  
 : FILING DATE: 07-JUN-1995  
 : CLASSIFICATION: 530  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/425,336  
 : FILING DATE: 18-APR-1995  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/064,691  
 : FILING DATE: 12-MAY-1993  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/986,430  
 : FILING DATE: 09-DEC-1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/901,707  
 : FILING DATE: 19-JUN-1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/787,567  
 : FILING DATE: 04-NOV-1991  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: McNicholas, Janet M.  
 : REGISTRATION NUMBER: 32,918  
 : REFERENCE/DOCKET NUMBER: 110220507/200-70.P3.C2A  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 312/707-8889  
 : TELEFAX: 312/707-9155  
 : TELEX: 650 388-1248  
 : INFORMATION FOR SEQ ID NO: 9:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 261 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : OS-08-488-113B-9

Query Match	84.2%	Score 667.5	DB 1	Length 261
Best Local Similarity	85.6%	Pred. No. 2.2e-72		
Matches 131	Conservative	9	Mismatches 12	Indels 1
				Gaps 1
QY	2	INITITDAAGNATINKATFTMESLRQADDPKCYGICIMLEDPTNSTPYLLVKIQGANK	61	
Db	1	INTITDAAGNATINKATFTMESLRQADDPKCYGICIMLEDPTNSTPYLLVKIQGASLK	60	
QY	62	TTTLMRRNNLLVYMGSDPFNGNKKRYHFFNDITESTDVENTLCSSSSRVAMSTNYN	121	
Db	61	TTTLMRRNNLLVYMGSDPEYD-NKCRYHFFNDIKTEYSDEVENTLCSNRPVAKPANYN	119	
QY	122	SLYPTMEKAEVNSRRNOVLGIQLISDGIKIS	154	

DB 120 GLYPTLEKKAQVTSRNEVOLGIQLSSDIGKIS 152

## RESULT 4

US-08-477-484B-9  
Sequence 9, Application US/08477484B

Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESSES:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-9

Query Match 84.2%; Score 667.5; DB 1; Length 261;

Best Local Similarity 85.6%; Pred. No. 2,2e-72;

Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 61

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 1 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 122 SLVPTMEKKAQVTSRNEVOLGIQLSSDIGKIS 154

## RESULT 5

US-08-646-360-9  
Sequence 9, Application US/08646360

Patent No. 5837491

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESSES:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-646-360-9

Query Match 84.2%; Score 667.5; DB 2; Length 261;

Best Local Similarity 85.6%; Pred. No. 2,2e-72;

Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 61

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

DB 2 INTITFDAGNATINKYATFMSLRNQAQPKLKYGIPLPPTNSTPKYLKVLKLOGANLK 60

Db 61 TTTLRRNNLYVMGYSDPYD-NKCRHYIFNDIKETESDVNTLCSSNPRVAKPINYN 119  
QY 122 SLYPTMEKAEVNSRNOVOLGIOLISSDICKIS 154  
120 GLYPTLEKKAGVTSRNEVOIGIOLISSDICKIS 152

RESULT 6  
US-08-839-765-9  
Sequence 9, Application US/08839765  
Patent No. 6146631

## GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

## ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155

## TELEFAX:

TELEFAX: 650 388-1248

## INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-839-765-9

Query Match

Best Local Similarity 84.2%; Score 667.5; DB 4; Length 261;

Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 62 TTTLRRNNLYVMGYSDFPFGNKCRHYIFNDITSTERTDVNTLCSSSSRVAMSIYN 121  
Db 61 TTTLRRNNLYVMGYSDPYD-NKCRHYIFNDIKETESDVNTLCSSNPRVAKPINYN 119  
QY 122 SLYPTMEKAEVNSRNOVOLGIOLISSDICKIS 154  
120 GLYPTLEKKAGVTSRNEVOIGIOLISSDICKIS 152

RESULT 7  
US-09-136-389-9  
Sequence 9, Application US/09136389  
Patent No. 6146850

## GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155

TELEFAX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-136-389-9

Query Match

Best Local Similarity 84.2%; Score 667.5; DB 4; Length 261;

Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

```

QY 2 INTFTDAGAAITNKATATMESLRNOKPKLCKGIGIMLPPTNSTPYLLVYKLOGAATLK 61
Db 1 INTFTDAGAAITNKATATMESLRNOKPKSLCKGIGIMLPPTNSTIYLLVYKLOGASLK 60
QY 62 TITLMLRRNNLYVMGSDPEPNCNKKCRHYHFNDITSTERTDYENTLCCSSSSRVAMSIYN 122
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 TITLMLRRNNLYVMGSDPYD-NKCRHYHFNDIKGTETSDVENTLCPSSNPRAKPIYNN 119
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 122 SLVPTMEKKAEVNSRNQVGLGIQLSSDICKIS 154
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 120 GLVPTLEKKAQVTSRNEVQLGIQLSSDICKIS 152

```

RESULT 8  
 US-09-610-838-9  
 : Sequence 9, Application US/09610838  
 Patent No. 6376217  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studulka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 City: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/610,838  
 FILING DATE: 06-JUL-2000  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE: 18-AUG-1998  
 APPLICATION NUMBER: 08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70, P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 368-1248  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 261 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

```

US-09-610-838-9
Query Match      84.2%; Score 667.5; DB 4; Length 261;
Best Local Similarity 85.6%; Pred. No. 2,2e-72;
Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1

QY      2  INTTFDAQNAATINKATFEMESLRQAADPKLCKYCGIMLPDPTNSTPKYLLVKKLOGANLK 61
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  INITTDACNATINKATFEMESLRQEAADPSLCKYCGIMLPDPTNSTIYLLVKKLOGASLK 60

QY      62  TITLMLRRNNLLVYMGSDPFNGNKKCRHAFNDITSEXTDYENTLCCSSSSRVAHMSNTYN 122
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  TITLMLRRNNLLVYMGSDPYD-NKCRHYHFNDIKETESVDVENTLCPSSNBRVAKPNTYN 119

QY      122  SLVPTMEKKAENVSRNVOVGIOILSSDGIKIS 154
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      120  GLVPTLEKKAQVTSRNEVVGIOILSSDGIKIS 152

```

```

1      RESULT 9
2      US-07-901-707-9
3      : Sequence 9, Application US/07901707
4      : Patent No. 5376546
5      : GENERAL INFORMATION:
6      : APPLICANT: Bernhard, Susan L.
7      : APPLICANT: Better, Marc D.
8      : APPLICANT: Carroll, Steve F.
9      : APPLICANT: Lane, Julie A.
10     : TITLE OF INVENTION: Materials Comprising and Methods of
11     : TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
12     : NUMBER OF SEQUENCES: 57
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
15     : ADDRESSEE: Bicknell
16     : STREET: Two First National Plaza, 20 South Clark
17     : STREET: Street
18     : CITY: Chicago
19     : STATE: Illinois
20     : COUNTRY: USA
21     : ZIP: 60603
22     : COMPUTER READABLE FORM:
23     : MEDIUM TYPE: Floppy disk
24     : COMPUTER: IBM PC compatible
25     : OPERATING SYSTEM: PC-DOS/MS-DOS
26     : SOFTWARE: Patentin Release #1.0, Version #1.25
27     : CURRENT APPLICATION DATA:
28     : APPLICATION NUMBER: US/07/901,707
29     : FILING DATE: 19920619
30     : CLASSIFICATION: 435
31     : PRIOR APPLICATION DATA:
32     : APPLICATION NUMBER: US 07/787,567
33     : FILING DATE: 04-NOV-1991
34     : ATTORNEY/AGENT INFORMATION:
35     : NAME: No. 5376546and, Greta E.
36     : REGISTRATION NUMBER: 35,302
37     : REFERENCE/DOCKET NUMBER: 27129/30910
38     : TELECOMMUNICATION INFORMATION:
39     : TELEPHONE: (312) 346-5750
40     : TELEFAX: (312) 984-5750
41     : TELEX: 25-3856
42     : INFORMATION FOR SEQ ID NO: 9:
43     : SEQUENCE CHARACTERISTICS:
44     : LENGTH: 261 amino acids
45     : TYPE: AMINO ACID
46     : TOPOLOGY: linear
47     : MOLECULE TYPE: protein
48     : US-07-901-707-9
49
50     Query Match      83.3%: Score 660.5; DB 1; Length 261;
51     Best Local Similarity 85.0%: Pred. No. 1.5e-71;
52     Matches 130: Conservative 9; Mismatches 13; Indels 1; Gaps 1;
53
54     2 INITPDAGNATINKKATFMESLRNOAKDPKLCYGIPIMLPDTNSTIPKVLKLOGCANLK 61

```

Db 1 INTITFDGAGNATINKYATFMSLRNEAKDPSLKCIGIPMLPNTSTIKYLLVKGASLK 60  
Qy 62 TITLMLRRNNLYVMGYSDPFNGKCRHYHFNIDISTERTDVENTLCCSSSSRVAMSINYN 121  
Db 61 TITLMLRRNNLYVMGYSDPYD-NKCRHYHFNIDIKTEYSDVENTLCPSSNPRVAKPINYN 119  
Qy 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154  
Db 120 GLYPTLEKKAAGVTSRNEVOLGIQLSSKIGKIS 152

RESULT 10  
US-07-988-430-9  
Sequence 9, Application US/07988430  
Patent No. 5416202  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Lane, Julie A.  
APPLICANT: Lei, Shau-ping  
TITLE OF INVENTION: Materials Comprising and Methods of  
PREPARATION and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/988,430  
FILING DATE: 19921209  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5416202and, Greta E.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-3750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-988-430-9

Query Match 83.3%, Score 660.5, DB 1: Length 261:  
Best Local Similarity 85.0%, Pred. No. 1.5e-71:  
Matches 130: Conservative 9; Mismatches 13; Indels 1; Gaps 1:  
Qy 2 INTITFDGAGNATINKYATFMSLRNEAKDPSLKCIGIPMLPNTSTIKYLLVKGASLK 61  
Db 1 INTITFDGAGNATINKYATFMSLRNEAKDPSLKCIGIPMLPNTSTIKYLLVKGASLK 60

Qy 62 TITLMLRRNNLYVMGYSDPFNGKCRHYHFNIDISTERTDVENTLCCSSSSRVAMSINYN 121  
Db 61 TITLMLRRNNLYVMGYSDPYD-NKCRHYHFNIDIKTEYSDVENTLCPSSNPRVAKPINYN 119  
Qy 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154  
Db 120 GLYPTLEKKAAGVTSRNEVOLGIQLSSKIGKIS 152

RESULT 11  
US-08-425-336-9  
Sequence 9, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
PROTEINS  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-9

Query Match 83.3%, Score 660.5, DB 1: Length 261:  
Best Local Similarity 85.0%, Pred. No. 1.5e-71:  
Matches 130: Conservative 9; Mismatches 13; Indels 1; Gaps 1:  
Qy 2 INTITFDGAGNATINKYATFMSLRNEAKDPSLKCIGIPMLPNTSTIKYLLVKGASLK 61  
Db 1 INTITFDGAGNATINKYATFMSLRNEAKDPSLKCIGIPMLPNTSTIKYLLVKGASLK 60  
Qy 62 TITLMLRRNNLYVMGYSDPFNGKCRHYHFNIDISTERTDVENTLCCSSSSRVAMSINYN 121  
Db 61 TITLMLRRNNLYVMGYSDPYD-NKCRHYHFNIDIKTEYSDVENTLCPSSNPRVAKPINYN 119  
Qy 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154



Db 120 GLYPTLEKKAAGVTSRNEVQGIQLISKIGKIS 152

## RESULT 12

PCT-US92-09487-9  
Sequence 9, Application PC/TUS9209487  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.  
APPLICANT: Belter, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Lane, Julie A.  
APPLICANT: Lei, Shau-Ping  
TITLE OF INVENTION: Materials Comprising and Methods of  
Preparation and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/09487  
FILING DATE: 19921104  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3836  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-09487-9

Query Match 83.3%; Score 660.5; DB 5; Length 261;

Best Local Similarity 85.0%; Pred. No. 1.5e-71;  
Matches 130; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

Db 120 GLYPTLEKKAAGVTSRNEVQGIQLISKIGKIS 152

RESULT 13  
US-08-373-858-2  
Sequence 2, Application US/08373858  
Patent No. 5633155

## GENERAL INFORMATION:

APPLICANT: Kim, Man-Keun  
APPLICANT: Lee, Kwan-Ho  
APPLICANT: Na, Byeong-Kook  
APPLICANT: Jeong, Han-Seung  
APPLICANT: Choi, Kyu-Whan  
APPLICANT: Moon, Young-Ho  
APPLICANT: Jeon, Hong-Seob  
TITLE OF INVENTION: Expression Vector for Phytolecta  
Activiral Protein and Process for Preparing Transgenic  
TITLE OF INVENTION: Plant Transformed Thereof.  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,858  
FILING DATE: 18-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Peter  
REGISTRATION NUMBER: 25,351  
REFERENCE/DOCKET NUMBER: 0136/17986-US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7770  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Phytolecta americana  
TISSUE TYPE: Leaf  
US-08-373-858-2

Query Match 75.2%; Score 596; DB 1; Length 313;

Best Local Similarity 71.9%; Pred. No. 1.2e-63;  
Matches 110; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

Db 120 GLYPTLEKKAAGVTSRNEVQGIQLISKIGKIS 152

RESULT 14  
US-08-500-611-2  
Sequence 2, Application US/08500611

Patent No. 5756322  
GENERAL INFORMATION:  
APPLICANT: Turner, Nilgun E.  
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,611  
FILING DATE: 11-JUL-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
TELEX: 139-125  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-500-611-2

Query Match 75.2%; Score 596; DB 1; Length 313;  
Best Local Similarity 71.9%; Pred. No. 1.2e-63;  
Matches 110; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFMSLRQAKDPKLCYGIPLDPTNSTPYLLVLOGANLK 61  
DB 23 VNTIIVNGSTTISKYATFLNDLRNEAKDPSLKCIGIMLPNTNPNKYVLELOGSNKK 82

QY 62 TTTLMLRRNNLYVWGYSDFPENGKCRHYIFNDISTERTDVENTLCSSSSRVAMSIYN 121  
DB 83 TTTLMLRRNNLYVWGYSDFPETNCRHYIFNDISCTERODVETTLCPNANSRVSKNINF 142

QY 122 SLVPTMEKKAENVSRNOVQIGIQLSDICKIS 154  
DB 143 SRYPTLESKAGVKSRSOVQIGIQLSDINIGKIS 175

RESULT 15  
US-08-500-694-2  
Sequence 2, Application US/08500694  
Patent No. 5880329  
GENERAL INFORMATION:  
APPLICANT: Turner, Nilgun E.  
TITLE OF INVENTION: DNA Encoding Pokeweed Antiviral Protein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500,694  
FILING DATE: 11-JUL-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
TELEX: 139-125  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-500-694-2

Query Match 75.2%; Score 596; DB 2; Length 313;  
Best Local Similarity 71.9%; Pred. No. 1.2e-63;  
Matches 110; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFMSLRQAKDPKLCYGIPLDPTNSTPYLLVLOGANLK 61  
DB 23 VNTIIVNGSTTISKYATFLNDLRNEAKDPSLKCIGIMLPNTNPNKYVLELOGSNKK 82

QY 62 TTTLMLRRNNLYVWGYSDFPENGKCRHYIFNDISTERTDVENTLCSSSSRVAMSIYN 121  
DB 83 TTTLMLRRNNLYVWGYSDFPETNCRHYIFNDISCTERODVETTLCPNANSRVSKNINF 142

QY 122 SLVPTMEKKAENVSRNOVQIGIQLSDICKIS 154  
DB 143 SRYPTLESKAGVKSRSOVQIGIQLSDINIGKIS 175

Search completed: July 2, 2003, 11:40:29  
Job time: 9.92767 secs